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ALIGNMENTS

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(c) 1993 - 2004 Compugen Ltd.
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		<pre>bukaryota's MetaZoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 537) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and</pre>	21C Frontier Korean EST Project 2001 Unpublished (2002) Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology	52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.
RESULT 1 BM832793 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT	

BM832793 K-EST0107 BI826605 603077056 BX108227 BX108227 CF780547 AGENCOURT

BM832793 BI826605 BX108227 CF780547

12 12 13 14

537 527 521 521

91.4 91.3 90.3 95.4

513 492 491.2 485.8

Query Match Length

Score

No. Result

Description

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/note="Organ: Drain: Vector: pCWV-SPORT6; Site 1: Not1; Site 2: EcoRv (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full:length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                              BI826605 527 bp mRNA linear EST 04-OCT-2001
603077056F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5168892 5',
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Life Technologies, Inc.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Cloe distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
    http://image.llh.gov
    Plate: LiAM1419 row: p. column: 13
    High quality sequence stop: 519.
    iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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421 CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                              91.4%; Score 492; DB 12; Length 527; 98.3%; Pred. No. 1.8e-100;
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Site_2: Not!; The poly (A)+ RAM was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector vas circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli POD10F' by electroporation method. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded RNA by in vitro transcription reaction. The synthesized RNA by in vitro transcription reaction. The synthesized RNA by in vitro transcription liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by
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Pred. No. 3.4e-105;
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CF780547 BOT 217 bp mRNA linear EST 20-OCT-2003 AGENCOURT 15739102 NIH MGC_217 Homo sapiens cDNA clone iMAGE:30524555 5', mRNA sequence.
                                                                                                                                                                                                                                61 AAATATGAGTTGGCGAGGAAGATCGACCTGTTATTGGCCTAGTCCAAGACGCTATGTACA 120
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Eukaryotta.

Mammalia; Butheria, Primates, Catarrhini, Hominidae; Homo.

(Dases 1 to 517)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
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                                                                                                                                                                                                                                                                                 137 GCCICCIGAAAIGAIIGGGCCTAIGCGGCCCGAGCAGIICAGIGAIGAAGIGGAACCCAGC
                                                                                                      CAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATTCATCTGTGTG
                                                                                                                                                                                           80 AAATATGAGTIGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGACGCTACGTAGA
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Bldg. 31 RmlOAD7 Bethesda, MD 20892
Bldg. 31 RmlOAD7 Bethesda, MD 20892
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The IM.A.G.B. Consortium (Linl.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/Linl at:
http://mage.llnl.gov.e column: 12
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                                                                   3;
                         521;
                         Length
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                     DB 13;
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Pred. No. 2.7e-100;
0; Mismatches 8;
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Location/Qualifiers
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                  91.3%;
97.9%;
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                                                            Conservative
           Query Match
Best Local Similarity
Matches 509; Conserv
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BX108227 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGp998K213161;
                                                                                                                  428
CAGGAGGAAGGATGAGGAAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGC 308
                                          241 CAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGC 300
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/note="Vector: PT73D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco H adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seg primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neubert, P., Partsch, E., Peters, M.,
                                                                                      CAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGCCAGGAG
                                                                                                                                                                             ATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAG
                                                                                                                                                                                                                                                                   TGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGGTCCTATGTTGGAAATTTGTTCATT
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RZPD; IMAGD998K213161.

Ruman Unigenest - RZPD3 (RZPDLIB, No.972)

http://www.rzpd.de/clonecards/cgi-
blishow.hib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenserlitum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Fax: +49 30 32639 101
                                                                                                                                                                                                                                                                                                                                                                      536
                                                                                                                                                                                                                                                                                                                                                                                                  AAAATTCTCCCAATAAAGCTTTACAG-CTTCTGCAAAGAAAAAAA 527
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Im Nevenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGp998K213161 , IMAGE:1256204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ebert, L., Heil, O., Hennig, S., Neuber
Radeloff, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
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xref="taxon:9606"
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BX108227
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298 AAGCICATAGCCAGGAACAGGGICACCCACAGACIGGGIGIGAGIGIGAAGAIGGICCIG 357
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/lab.host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_990"
/clone_lorgan_liver; Vector: pcWV-SPORT6; Site_l: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                  Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 AAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Thc.
Clone distribution: MGC Clone distribution information can k
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llh.gov
Plate: LiAM12026 row! I column: 24
High quality sequence stop: 509.
High quality sequence stop: 509.
                                                                                                                Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                           Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo
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98.0%;
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Mammalia; Eutheria;
1 (bases 1 to 509)
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                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db.xref="taxon:9606"
/clone="type="Pooled Chondrosarcoma Tumor cells"
/lissue_type="Pooled Chondrosarcoma Tumor cells"
/lissue_type="Pooled Chondrosarcoma Tumor cells"
/lissue_type="Thing (Ti phage-resistant)"
/clone lib="NHH MGC 217"
/note="Vector: pXx-Asc; Site_1: BCoRI; Site_2: NotI;
/list strand cDNA was size fractionated on a 1% agarose gellonatured RNA was size fractionated on a 1% agarose gellonatured CDNA was size fractionated on a 1% agarose gellonatured CDNA was size selected according tomRNA size fraction, ligated with EcoR I adaptor; digested with Not I and then cloned directionally into pXX-Asc vector. Average insert size 0.5-1xb. Adaptors 5'(AATTGGCAGAGGG)3' and 5'd and 5'd CCCCGTGGCGG)3'. 3' Linker sequence - GCGGCCGTGAGAGCC TI8. Sequencing primers 3'end: T3 promoter primer 5'd (TAATAGCGCTCATAAAGGGG)3'. Average insert size 0.5-1xb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 GGAGGGGAGGATGAGGGAGCATCTGCAGGTCAAGGCCGGAAGCCTGAAGCTCATAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 TGTACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 485.8; DB 14; Length 517;
Pred. No. 4.5e-99;
); Mismatches 7; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516
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BI868671
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/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled, Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-322087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWS10753 457 bp mRNA linear EST 03-MAR-2000 hd39d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. ;
                                                                                                   339
                                                                                                                                                                                 AGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGGCAAATCCAGAGGAGGTGAAAA 399
              400 CGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAG 459
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                       GTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTG
                                                                                                                                                                                                                                                                                                                                                                     460 GCTGCTCCTAIGTIGGAAAITIGTICAITAAAAITCTCCCAAIAAAGCTITACAGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-GGAP http://www.ncbi.ulm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                       130 CGCCTGAAGAAGGTGAAAAGCAATCACAGTTTAAAAGAAGGCACGTTGAAATGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                       70 GCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTTACAGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2911881"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW510753.1 GI:7148831
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AW510753
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Best Local Similarity
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                                                                                                                                     AA447559 489 bp mRNA linear EST 04-JUN-1997 zw81ell.sl Soares testis_NHT Homo sapiens cDNA clone IMAGE:782636 3' similar to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /close_lib="Soares testis NHT"
//note="Woctor: pT7T3D-Pac (Pharmacia) with a modified
foots="Woctor: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pyrv3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 489)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Mhote,Y., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGITACCAATCIGAAGIGGGAGCGGCCGCCAATTITITITITITIT 3/].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty_free through LLNL ; contact the
IMAGE Consortium (info@mage.llnl.gov) for further information.
Seq primer: -41ml3 Fwd. ET from Amersham
High quality sequence stop: 427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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                                                                                            RESULT 6
AA447559/c
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Anatomia tonical institute, cancer consider frozerow, reduced to the fortast institute, cancer contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation. M. Bento Soares, Ph.D.

CDNA Library Preparation. M. Bento Soares, Ph.D.

CDNA Library Preparation. Only erselyty Genome Sequencing Center

CLONE distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llh.gov/bbry/mage/image.html

Insert Length: 511 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham

High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMAJSGUS/ 464 bp mRNA linear EST 22-JAN-1998 mX15e11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence. AA738037
                                                                                                                                                                                                                                                                                                                                     CACAGACTGGGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGGCCAAATC 384
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 464)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACC
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                                                                                                                                                                                                                                                         GTTGGCGAGGAAGATCGACCTATATTGGCCTAGACCAAGGCGCTATGTACAGCCTTCTG
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                                                                                                                                                                          3;
                                                                                                                                  Length 447;
                                                                                                                                                                            Indels
                                                                                                                                    DB 9;
                                                                                                                                  Score 424.6; DB 9
Pred. No. 2.8e-85;
                                                                                                                                                                            0; Mismatches
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ilarity 98.4%;
Conservative
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/lab host="DH10B"
/clone lib="Soares_NFL_T_GBC_S1"
/clone="Organ: pooled" Vector: pT773D-Pac (Pharmacia) with
/note="Organ: pooled" Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH119W, testis NHT, and B-cell
NCI_GAP_GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
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                                                          398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493
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I (bases 1 to 47)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index (1997) Unpublished (1997) Uncontact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LiNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 497 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI381509 447 bp mRNA linear EST 28-MAR-:
te76b07.x1 Scares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGAAGACACGTTGAAAATGAAGCAGCTGCTCCTATGTTGGAAATTTGTTCATTAAAAT
                                                                                                     134 AGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGGGCAGTTCAGTGAAGTGGAACC
                                                                                                                               GGGAGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGA
                                                                                                                                                                                                                                                                                                               GGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGA
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                 GTGAAATATGAGTTGGCGAGGAAGATCGACCTATC---GGCCTAGACCAAGACGCTACGT
                                          AGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAAA 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2092597"
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Location/Qualifiers
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/clone_lib="LBSCKO"
hote="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: NoLI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lemnon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW016546 418 bp mRNA linear BST 10-SEP-1999 UI-H-BIOP-abg-g-06-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711986 3', mRNA sequence.
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                                                            Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Fmail: yongswall.kribb.re.kr Phate: 8 row: B column: 09
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Pred. No. 3.7e-83;
0; Mismatches 13
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                                                                                                                                                                                                                             organism="Homo sapiens"
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High quality sequence stop: 505.
Location/Qualifiers
                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L8SCK0-8-B09"
                                                                                                                                                                                                                                                                                                                      cell_line="SCK"
lab_host="Top10F'"
                                             Genome Research Center
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AW016546.1 GI:5865303
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96.5%;
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                            Contact: Kim YS
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                                                                                                                                        /clone_lib=_WIGI_CGAP_GG3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405
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                                                                                                                                                                                                                                                                                                                                                     Length 464;
                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                            tissue type="pooled germ cell tumors" lab host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                 Score 424.4; DB 9;
Pred. No. 3.1e-85;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21C Frontier Korean EST Project 2001
                                    'organism="Homo sapiens"
                                                                                           /clone="IMAGE:1256204"
                                                     'mol_type="mRNA"
'db_xref="taxon:9606"
 Location/Qualifiers
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K-EST0159805 L8SCK0 Homo
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Best Local Similarity 96.9%;
Matches 444; Conservative
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                                                                                                                                                                                                                                                                                                                                Email: cgapBs-r@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 418) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 7.5e-83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2711986"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                          'organism="Homo sapiens"
                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                       Seg primer: Mi3 Forward POLYA=Yes.
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99.5%;
sapiens (human)
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                                                                                                Unpublished (1997)
                                                                                      Tumor Gene Index
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602553732F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:4451958 5',
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                                                                                                                                                                                                                                                                                                                                                                                                     358 IGAAGIGGAACCAGCAACACCTGAAGAGGGGAACCAGCAACTCAACGTCAGGATCCTGC 299
                                                                                                                                                                                                                                        298 AGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAAACGCCTGAAGAAGGTGAAAAGCA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 ATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host_bhild (phage_resistant)"
/clone lib="NIH MGC 90"
/clone lib="NIH MGC 90"
/clone lib="NIH MGC 90"
site_1 sall; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ATCACAGTGTTAAAAGAAGCACGTTGAAATGATGATGCAGGCTGCTCCTATGTTGGAAATTT
                                                                                                                                                                                                                                                                                                                         302 TCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGG
                                                                                                                                                            AGCTGCTCAGGAGGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.8%; Score 413.4; DB 12; 97.4%; Pred. No. 9.3e-83; ive 0; Mismatches 11; I
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/db_xref="taxon:9606"
/clone="IMAGE:4451958"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 bp mRNA linear EST 16-MAR-1998 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245 to SW:GGEZ_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
information can be
                                                                 GAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGAGGGAACCAGCAACTCAA 227
                                                                                                                                                                                                   CCGAAGCCIGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAA 347
                                                                                        CGTCAGGAICCTGCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGG 287
                                                                                                                                                            CGTCAGGATCCTGCAGCTGCTCAGGAGGGAGGGATGAGGACGAGCATCTGCAGGTCAGGG 194
                                                                                                                                                                                                                            CCGAAGCCTGAAGCTGATAGCCAGGAACAGGCTCACCCACAGACTGGGTGTGAGTGTGAA 254
                                                                                                                                                                                                                                                                               407
                                                                                                                                                                                                                                                                                                  GATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA 314
                                                                                                                                                                                                                                                                                                                                       GAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGATGCAGGCTGCTCC 467
                                                                                                                                                                                                                                                                                                                                                              TAIGITGGAAATITGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTTACAGCCTTCTTGCAAAA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCC
                     GATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLML at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. BT from Amersham High quality sequence stop: 363.

Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:1409245"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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COMMENT

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Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified py773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified Dolylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mNNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA760996 450 bp mRNA linear EST 26-JAN-1998 nx32h08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAGAGGGAACCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGACCTATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 IGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 TGCTCCTATGTAGGAAATTTGTTCATTAAAATTCTCCCAATAAAACTTTACAGCCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 412.8; DB 9; Length 426; 97.9%; Pred. No. 1.3e-82; live 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bmail: cgapbs-remail.nih.gov
Issue Procurement: Christopher A. Moskaluk, M.D., i
Emmert-Buck, M.D., Ph.D.
cDNa Library Preparation: M. Bento Soares, Ph.D.
cDNa Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA760996.1 GI:2809926
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Unpublished (1997)
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Fatima

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/lab_host="DH10B"
/clone lib="Soares testis NHT"
/note="Vector: pryT310-pac"(Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratozies, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                        CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Clone distribution: NCI-CGAP clone distribution information can be
Clone distribution: NCI-CGAP Clone distribution information can be
Cloud through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/TI vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
I (bases 1 to 45. No. No. No. No. No. No. CARP http://www.nobi.nlm.nih.gov/noicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAAGCAATCCCAGTGTTAAAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455 AIGAGITGGCGAGGAAGATGACCTTATTTGGCCTAGACAAGGCGCTATGT-CAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 CIGAAAIGAIIIGGCCCTAIGCGGCCCCGAGCAGIICAGTGAAGGGGGGAACACCAGCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 CTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCCTGCAGGAGGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 ACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGCAGGAGATGGACCCGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 ACCCACAGACTGGGGTGTGAGGTGGAGATGGTCCTGATGGGGCAGGAGATGGCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 ATCCAGAGGAGGTGAAAAGGCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 ATGAGTTGGCGAGGAAGATCGACCTAT--CGGCCTAGACCCAAGACGCTACGTAGAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 CTGAAATGATTGGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 ATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 455;
                                                                                                                                                                                       Email: cgapbs-romail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M.
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:1751408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                             Tumor Gene Index
Unpublished (1997)
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Best Local Similarity
Matches 435; Conserv
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TITLE
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                                                                                                                                                                                                                                                                                     /tissue type="pooled germ cell tumors"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GC4"
/clone_lib="NCI_CGAP_GC4"
/note="vector: pT713D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo (dT) primer. Double-stranded cDNA was ligated to Eco
nigo (dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
              DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAAGAAG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 ACACGITGAAAIGAIGCAGGCIGCICCIAIGITGGAAAITIGITCAITAAAAITCICCCA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 ACACGITGAAATGATGCAGGCTGCTCCTATGTTGGAAAITTGTTCATTAAAATTCCCA
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                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                              /clone="IMAGE:1257855"
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ilarity 97.3%;
Conservative C
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(c) 1993 - 2004 Compugen Ltd.
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nucleic search, using sw model ı OM nucleic

8, 2004, 09:50:03; Search time 372 Seconds (without alignments) 6143.899 Million cell updates/sec August Run on:

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1 ACGCCAGGGAGCTGTGAGGC......CTGCAAAGAAAAAAAA 538 Perfect score: Sequence:

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3373863 seqs, 2124099041 residues Searched:

5017792 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 538 Minimum DB Maximum DB

Post-processing: Minimum Match 08
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Listing first 45 summaries

N_Geneseg 29Jan04:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

Lung canc Human sec Human can Aax90519 GAGE-2 tu Abz20463 GAGE-2 fu Ada15801 Human GAG GAGE-5 tu CDNA enco Lung cand Human bla Human GAG Description Abz20463 (Ada15801)
Aax90522 (Abl66323)
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Abx76236)
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Abz20480 TPS1 subt	Abz18686 Group III	Abz19538 Group III		Aas69484 DNA encod	Abt15728 Human can	Aad14981 Human NOV						Ade72125 Human lun	Aad24228 Human dif			Aas63900 Human pro	Aah02872 Prostate	_			
ABZ20480	ABZ18686	ABZ19538	AA160530	AAS69484	ABT15728	AAD14981	ABT15736	AAF68151	ABK38062	ACA10391	ABX99342) ADE72125		ABA92217	AAH93807	AAS63900	AAH02872	AAH85121	ACA59708	ABL95271	ACC95435
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7	c 25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

BP. AAX90519 standard; cDNA; 538 entry) (first 30-SEP-1999 AAX90519; RESULT 1 AAX90519

GAGE-2 tumour rejection antigen clone nucleotide sequence.

Human leukocyte antigen, HLA-A29; tumour rejection antigen, detection, therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte; GAGE; ss.

Homo sapiens

WO9937665-A1

29-JUL-1999.

99WO-US000775. 12-JAN-1999;

98US-00012818, 23-JAN-1998; (LUDW-) LUDWIG INST CANCER RES

Boon-Falleur T; Debacker O, ъ, Van Den Eynde Van Der Bruggen P,

WPI; 1999-469111/39.

New isolated peptides which bind to HLA-A29 molecules, which are tumor rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.

Example 13; Fig 4; 62pp; English.

The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE timour rejection antigen clone, from an example from the present invention

Human can Group III Group III Group III Group III Human can

Abz19533 Abz19955 Abz19755 (Abz19551 (

ABZ19533 ABZ19955 ABZ19755

55.6 44.9 41.8

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U υ Human GAG Human cDN TPS1 subt

Acd42232 Adc24646 Abz20497 Abx77605 Abt15737

ACD42232 ADC24646 ABZ20497

4BX77605

520 509 509 509 229

411.3 40.3 38.8 38.8 38.8

209 209 206.6

ABZ19551

Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;

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Pred. No. 6e-146;
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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ABP5446 to ABP54472 represent isolated polynucleotide (I) sequences, and ABP54446 to ABP54472 represent protein (II) sequences, from the present tinvention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 1.3e-143;
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New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic Tlymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte antigen (HLA) molecule. The GAGE-TB and GAGE-B and cleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents cDNA encoding the human GAGE-B polypeptide of the invention. The gene resides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATCGGCCTAGACCAAGACGCTAC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATCGGCCTAGACCAAGACGCTAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
      numman; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL; human leukocyte antigen; HLA; tumour rejection antigen precursor; major histocompatibility complex; MHC; cytolytic T cell proliferation; chromosome Xpl1.2-pl1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIGITATION CONTROLL CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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aa:Lys)
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Pred. No. 2.7e-142;
                                                                                                                                                                                                                                                                                                                                                                      /transl_except= (pos:244. .246, /transl_except= (pos:400. .402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boon-Falleur
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                                                                                                                                                                                                                                                                                                                                             GAGE-8"
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/product= "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Col 7-10; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00163748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00163748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on chromosome Xp11.2-p11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526; Conservative
                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-401119/38.
P-PSDB; ADA15778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6509172-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
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                                                                                              360
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                                                               371
                                                                                                                            431
                                                                                                                                                         420
                                                                                                                                                                                          491
                                                                                                                                                                                                                      421 TAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                  GAGGGAAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATGACCTAA
                                                                                      301 GAACAGGGTCACCCACAGACTGGGGTGTGAGATGGTCCTGATGGTCCTGATGGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection;
GAGGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTCATAGCCAG
                                                              GAACAGGGTCACCCACAGACTGGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATG
                                                                                                                         GACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGAGAAAAAGCAATCACAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor
                                                                                                                                                 361 GACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGT
                                                                                                                                                                                       TAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection therapy; pathological condition; cancer; CTL; cytolytic I lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated peptides which bind to HIA-A29 molecules, which are rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boon-Falleur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.8%; Score 504.8; DB 2; Length 532; 98.1%; Pred. No. 2.7e-136; 1ive 0; Mismatches 7; Indels 3.
                                                                                                                                                                                                                                                       538
                                                                                                                                                                                                                                                                                    527
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGE-5 tumour rejection antigen clone nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   492 AITCICCCAAIAAAGCITIACAGCCTICIGCAAAGAAAAAAAAA
                                                                                                                                                                                                                                                                                 Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Den Eynde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Fig 4; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                            AAX90522 standard; cDNA; 532
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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AGCTGTGAGGCAGTGCTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT

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25-SEP-2000; 2000US-0235280P.
26-SEP-2000; 2000US-0235633P.
27-SEP-2000; 2000US-0235633P.
27-SEP-2000; 2000US-0235711P.
27-SEP-2000; 2000US-023570P.
27-SEP-2000; 2000US-0235863P.
28-SEP-2000; 2000US-023688P.
28-SEP-2000; 2000US-023603P.
28-SEP-2000; 2000US-023603P.
28-SEP-2000; 2000US-023603P.
28-SEP-2000; 2000US-02369P.
28-SEP-2000; 2000US-0236111P.
28-SEP-2000; 2000US-023691P.
28-SEP-2000; 2000US-023691P.
28-SEP-2000; 2000US-023691P.
28-SEP-2000; 2000US-023691P.
28-SEP-2000; 2000US-023691P.
28-SEP-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-0237316P.
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2000US-0244867P.
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Best Local Similarity 98.3
Matches 518; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Augustus M,
                                                                                                                                                                                                                                                                                                                                                                                                 Weaver Z;
                                                                                                                                                                                                                                                                                                                                                             (AVAL-) AVALON PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                  03-OCT-2000;
                                                                                                                                                                                                                                                                                                             03-OCT-2000;
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Soppet DR,
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                                                                                                                                                                                                                                                                                                                                                              480
                                                                                        186
                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 AGCTGTGAGGCAGTGCTGTGTGCTGCCGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
                                       CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGAC
                                                           CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC
                                                                                        GCTACGTAGAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCCGAGCAGTTCAGTGATGAAG
                                                                                                                                                                TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                              241 CTCAGGAGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGGAAGCCTGAAGCTGATA
                                                                                                                                                                                                                                       GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGCCAGG
                                                                                                                                                                                                                                                      AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC
                                                                                                                                                                                                                                                                                                     AGATGGACCCCCCABATCCAGAGGAGGGGGGAAAACGCCTGAAAGAAGGTGAAAAGGAATCAC
                                                                                                                                                                                                                                                                                                                                     AGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
                                                                                                                                                                                                                                                                                                                                                             AGTETTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
                                                                                                               121 GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
                                                                                                                                        TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                        CTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTCATA
                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer related gene sequence SEQ ID NO:4660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-2000; 2000US-0233133P.

18-SEP-2000; 2000US-0233617P.

20-SEP-2000; 2000US-0234039P.

20-SEP-2000; 2000US-0234434P.

20-SEP-2000; 2000US-0234509P.

22-SEP-2000; 2000US-0234509P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL66323 standard; DNA; 528 BP.
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2000US-0209531P.
2000US-0233133P.
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2000US-0234034P.
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2000US-0235082P.
2000US-0235134P.
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25-SEP-2000; 2000US-0234923P.
25-SEP-2000; 2000US-0234924P.
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25-SEP-2000; 2
25-SEP-2000; 2
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The present invention userings a method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 8447 sequences (given in ABIG1664 to ABI70110), or is at least 95% identical to (S), where a change in comprises in indicative of anti-neoplastic activity. (I) has eyeostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocationma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method (M1) for screening for an anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG
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Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 528;
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Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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    Ebner
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associated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with a polynucleotide
that selectively hybridises to a sequence that is 80 % identical to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from a
patient with
  ACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAG
                                                                                                                                          AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGA
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                                                                                                       TGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCC
                                                                                                                                                                                                            TGCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA sequence SEQ ID NO:144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a bladder cancer-associated transcript in a cell patient, comprises contacting a biological sample from the bladder cancer-associated polynucleotide or antibody.
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2001US-0343705P.
2001US-0350666P.
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08-NOV-2001;
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table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 and code the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lung cancer-associated polynucleotide, gene, ds, cytostatic, emphysema, antiinflammatory, antiasthmatic; non-small cell lung cancer; atelectasis, small cell lung cancer; benign lesion, precancerous lesion, bronchitis, chronic obstructive pulmonary disease, hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                         Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                             DB 7;
                                                                                                                                                                                                                                                             Score 498.8; DB 7;
Pred. No. 1.5e-134;
0; Mismatches 7;
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                                                                                                                                                                                                                                                             92.78;
                                                                                                                                                                                                                                                                            98.1%;
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nes 516, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                        Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGGGAGCTGTGGGCTGTGTGGTTCCTGCCGCACTCTTTTCCTCTAC
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2001US-0339245P.
2001US-0350666P.
2001US-0334370P.
2002US-0372246P.
                                                                                                                                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC.
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P-PSDB; ABU56512.
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     WO200286443-A2.
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09-NOV-2001;
                                                                          18-APR-2002;
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                                                                                                           18-APR-2001;
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                                      31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid encoding GAGE tumour rejection antigen precursor processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas.
                                                               GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAG
                                                                                                                                                       CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGAAGGCTGCTCCTATGTTGGAAAT
genganagecaggaacagggncacccacagacngggngngagngngaaganggncengan
                                        GGGCAGGAGATGGACCCGCCAAATCCAGAGGTGAAAACGCCTGAAGGAGGTGAAAAG
                                                                                                                       CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In
                                                                                                                                                                                                      525
                                                                                                                                                                                                        TIGITICATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAA
                                                                                                                                                                                                                                      481 TIGITCATIAAAATICICCCAATAAAGCITITACAGCCITCIGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding GAGE-5 tumour rejection antigen precursor.
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/transl_except= (pos:189. .191, aa:Ala)
/transl_except= (pos:192. .194, aa:Thr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   BP.
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.197, aa:Thr)
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Pred. No. 5.6e-134;
0; Mismatches 12;
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precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or unith can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence encodes a GAGE-2 tumour tumour rejection antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated GACB-7B and GACB-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte antigen (HLA) molecule. The GAGE-8 nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents cDNA encoding the human GAGE-7B polypeptide of the invention. The gene resides on chromosome Xp11.2-p11.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
                535
                                                                                                                                                                                                   Human, GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL; human leukocyte antigen, HLA; tumour rejection antigen precursor; major histocompatibility complex; MHC; cytolytic T cell proliferation; chromosome Xp11.2-p11.4.
                                                                                                                                                                                                                                                                                                                                                            aa: GPMRPEQGSDEVPEMI)
aa: HPQTGKPEAHSQEQ)
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 488; DB 7; Length 526;
Pred. No. 2e-131;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                            .162,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boon-Falleur
                                                                                                                                                                                                                                                                                                                                            /product= "Human GAGE-7B"
/transl_except= (pos:115.
/transl_except= (pos:265.
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Col 9-10; 15pp; English.
                                                                                      BP.
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                                                                                                                                               entry)
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                                                                                    ADA15802 standard; cDNA;
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                                                                                                                                             (first
                                                                                                                                                                         Human GAGE-7B cDNA,
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                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Backer O,
                                                                                                                                                                                                                                                                                                                                                                                                        US6509172-B1
                                                                                                                                             06-NOV-2003
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                                                                                                                 ADA15802;
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GGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTCATAGCCCAGGAACAGGGTCACCCA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCA 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tag; secreted protein; cDNA isolation;
TGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAA
                                             ATGATTGGGCCTATGCGCCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAA
                                                                                                                                                                                               ATGATTGGGCCCTATGCGGCCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAA
                                                                                                                                                                                                                                                                                           GAAGGGGAACCAGCAACTTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGAAGGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein 5' EST, SEQ ID NO: 2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTACAGCCTTCTGCAAAGAAAAAAAA 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ą,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-500381/45.
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P-PSDB; AAG02123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
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derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGAGATICATCTGTGAAATATGAGTTGGCGAGGAAGATCGACCTAT--CGGCCTAG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
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squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
Lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 ACGCCAGGGAGCTGTGAGGCAGTGCTGTGTGCTTGCTGCCGTCCGGACTCTTTTTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATNAYGGCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 AGCICATAGCCAGGAACAGGGTCACCACAGACTGTGAGTGTGAAGATGGTCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATGAAGTGGAACCAGCAACACCTGAAGAAGAGGGAACCAAGCAACTCAAGGATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 357.8; DB 3; Length 430;
Pred. No. 1.3e-93;
5; Mismatches 2; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGCAGGAGATGGACC 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.5%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS60104 standard; cDNA; 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used as terested to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemocherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel cancer transcripts or genomic sequences corresponding to the cast cancer. Probes based on the markers can be used to treat cancer. Probes based on the markers can be used to cancer agents developed by the novel cased to detect transcripts or genomic sequences corresponding to the carting of the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmcoytoma, reticulum cell sarcoma, Hodgkin's control cancer cell markers
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                                                                                                  nucleic acid, used as a marker to determine the effectiveness of TAXOL to treat cancer cell growth in individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 AGTGATGAAGTGGAACCAGC~-AACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 Arccignadcigencadnadganaggarnaggangcarnigenaggrengaggecogaage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 GAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;
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                     Van Huffel
                                                                                                                                                            Claim 1; Page 120; 527pp; English.
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                     Bolt A,
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                 Brown JL,
                                                         WPI; 2001-602933/68
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les 320; Conserv
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                   Lillie J,
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ID AAS6049
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AC AAS604:
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                                                                                                  Novel
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Matches
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cancer cert storm in an interviewer, the mainters can be used as cargets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous protein. Cancers which may be targeted include carcinoma (e.g. squamous leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets
                                  Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma; squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia; lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma; Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 GETCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCCCAGACTGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTGTGAAGATGGTCCTGATGGCCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 GGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid, used as a marker to determine the effectiveness using TAXOL to treat cancer cell growth in individuals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 299.2; DB 4; Length 365; Pred. No. 1.3e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 365 BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Van Huffel C;
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                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Human cancer agent-sensitive marker #227
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                                                                                                                                                                                                                                                                                                                                                                                                                         Bolt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.6%;
95.9%;
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Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Brown JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-602933/68
                                                                                                                                                                                                   WO200179556-A2
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                               25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         Lillie J,
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AB017575 to AB020506 represent isolated polynucleotide (I) sequences, and ABP5446 to AB05472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be present therapy and vaccines. (I), (II), artibodies and compositions in gene present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen; immune response; virology; immunology; microbiology; molecular biology; recombinant DNA technology; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 259 BP; 63 A; 65 C; 76 G; 55 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Group III cDNA cancer related clone SEQ ID NO:2217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2217; 207pp; English.
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538
                                                                                                                                                                                                                             ABZ19791 standard; cDNA; 259 BP
                                  519 CTGCAAAGAAAAAAA
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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09-JAN-2002;
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ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and ABP54446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antispens. They are useful for stimulating immune response. They can also be useful in virology microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
137 CAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTACAGTG 196
                                  ATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCCAGCAACTCAAGGTCAGGATCCTG 240
                                                     New immunogenic polynuclectides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA
                                                                                                                                                                                                                                                                                                                                                  Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
immune response; virology; immunology; miorobiology; molecular biology;
recombinant DNA technology; gene; ss.
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                                                                                                                                                                                                                                                                                                                  Group III cDNA cancer related clone SEQ ID NO:1959.
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
                                                                                                                                                                                                                   ABZ19533 standard; cDNA; 225
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79 GAAATATGAGTTGGCGAGGAAGATCGACCTATCGGCCTAGACCAAGACGCTACGTAGAGC 138

1 GCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATTCATCTGTGT 19 GCAGTGCTGTGGTTCCTGCCGGACTCTTTTTCCTCTACTGAGATTCATCTGT

78 09

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Length 225; 0; Indels

41.8%; Score 225; DB 7; I 100.0%; Pred. No. 3.7e-55; ive 0; Mismatches 0;

Conservative

Local Similarity

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Query Match

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121 Crccrgaaardarraggccrargcggcccgagcagrrcagrgaagagaagagcagcaa 180
CTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAA
                                                                                                  CACCTGAAGAAGGGGAACCAACTCAACGTCAGGATCCTGCAG 243
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Boon-Falleur, r. Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 (bases 1 to 538)
van der Eruggen, P., van den Bynde, B., DeBacker, O. and
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Sequence 14 from patent US 5858689.
AR028488
AR028488.1 GI:5940461
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1 ACGCCAGGGAGCTGTGAGGC.......CTGCRAAGAAAAAAAA 538
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Homo sapi Sequence

Sequence

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Homo sapi Sequence

Sequence Sequence Sequence

Sequence Sequence

PAT 29-SEP-1999

DNA

155851 Sequence 14
BD133467 Isolated,
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AX2415772 Sequence
AX316881 Homo sapi
AX911711 Sequence
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AR028488 Sequence BD231797 Isolated

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Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and their
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                                                                 molecules encoding the same, and utilization thereof
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PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 polypeptides binding with HLA-A29 molecule, nucleic acids as an endeanes encoding the same, and utilization the
                                                                                                                               'organism≈'Homo sapiens (human)'
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Location/Qualifiers
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Sequence 14 from patent US 5648226.
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/db_xref="taxon:9606"
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FEATURES
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TITLE
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E. 1 (bases 1 to 538)

S. Bruggen, P. V.D., Bynde, B. V.D., Debacker, O. and Falleur, T.B.
Isolated polyPeptides binding with HIA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof LUDWIG INSTITUTE FOR CANCER RESEARCH
OS. Homo sapiens (human)
P. D. 02-APR-2002
PR 12-UAN-1999 JP 2000528586
PR 12-UAN-1999 US 2000528586
PR 13-UAN-1999 US 09/012818
PI PIERRE VAN DER BRUGGEN, BENOIT VAN DEN BYNDE, OLIVIER DEBACKER, PI THIERRY DOON FALLEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD231797 538 bp DNA linear PAT 17-JUL-2003 Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.
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      Patent: US 5858689-A 14 12-JAN-1999;
                                           1. .538
/organism="unknown"
/wol_type="unassigned DNA"
                            Location/Qualifiers
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JP 2002509859-A/7.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.0
Matches 538; Conservative
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PD 05-MAR-2002
PP 05-MAR-2002
PP 23-UJN-1997 JP 1998503430
PR 24-UJN-1996 08/669161
PR 24-UJN-1996 08/669161
PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC A61X38/00, A61X45/05, C07X7/00, C07X14/82, C12N15/00 CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    artificial sequences.

1 (bases 1 to 538)

Debacker,O., Eynde,B.V.D. and Falleur,T.B.
Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof Patent: JP 2002507112-A 7 05-MAR-2002, hubblig institute FOR CANCER RESEARCH
                                                                                                                                                                                 CAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCGAGCAGTTCAGTG
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Pred. No. 2.6e-123;
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                                                           0; Mismatches
/mol_type="unassigned DNA
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JP 2002507112-A/7.
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Matches 538; Conservative
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For Cancer Research, 74 Avenue Hippocrate, BRUSSELS, 1200, BELGIUM
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1. Cases 1 to 530)

Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.

A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma

J. Exp. Med. 182 (3), 689-698 (1995)
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/organism="Homo sapiens"
/mol_type="genomic DNA
/db_xref="taxon:32630"
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Location/Qualifiers
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larity 100.0%;
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Direct Submission
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1 (bases 1 to 528)

1 (bases 1 to 528)

2 Backer, O., Arden, K. C., Boretti, M., Vantomme, V., De Smet, C., Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van de Bynde, B., Boon, T. and van der Bruggen, P.

Characterization of the GAGE genes that are expressed in various
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Direct Submitted (24-MRR-1998) Ludwig Institute for Cancer Research,
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
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                                                             DB 6;
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Pred. No. 3.5e-120;
0; Mismatches 1;
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/organism="Homo sapiens"
/organism="unknown"
/wol_type="genomic DNA'
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Location/Qualifiers
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AF055473.1 GI:3511022
                                                             97.7%;
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Homo sapiens
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                                                                                                                              /protein id="AAA82745.1"
/db_xref="G1:914901"
/translation="MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGE
PATQRQDPAAAQEGEDEGASAGQGFKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPE
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De Backer,O., Van den Eynde,B. and Boon-Falleur,T.
Isolated, truncated nucleic acid which are members of uses thereof
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ilarity 100.0%; Pred. No. 2.5e-121;
Conservative 0; Mismatches 0;
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Location/Qualifiers
1. .528
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                    /sex="female"
/cell_line="MZ2-MEL.43"
/tissue_type="melanoma"
/dev_stage="adult"
84. .434
                                                                                     84. "434"
/codon_start=1
/product="GAGB-2 protein"
        xref="taxon:9606"
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FEATURES
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Smet,C., Van den

PRI 01-MAY-2000

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BD231800 532 bp DNA linear PAT 17-JUL-2003 Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.
                                                                                                                                                                CATCTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGAC 126
                                                                                                                                                                                                                                                      Homo sapiens (human)
JP 2002509859-A/10
02-APR-2002
12-JAN-1999 JP 2000528586
23-JAN-1999 US 09/012818
PIERRE VAN DER BRUGGEN, BENOIT VAN DEN EYNDE, OLIVIER DEBACKER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 512)
Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, F.B. Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof Patent: JP 2002509859-A. 10 02-ARR-2002; LUDWIG INSTITUTE FOR CANCER RESERACH
                                                                                                                                                                                                                                                                                                                         181 TGGAACCACCAACACCTGAAGAAGAGAAACCAGCAACTCAACGTCAAGGATCCTGCAGGTG
                                                                                                 10 AGCTGTGAGGCAGTGCTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
                                                                                                                                 AGCTGTGAGGCAGTGCTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTTACTGAGATT
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                                                                   Indels
                                   Score 504.8; DB 6;
Pred. No. 4.8e-115;
0; Mismatches 7;
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                                 Query Match
Best Local Similarity 98.1%;
Matches 522; Conservative
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PATGRQDPAAAQEGEDEGASAGQGPKPRADSQEGGHPQTGCECEDGPDGQEMDPPNPE
EVKTPEEGEKQSQC"
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Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
Patent: US 5858689-A 17 12-JAN-1999;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      TCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATCGGCCTAGACCAAGACGCTAC
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van der Bruggen, P., van den Eynde, B., DeBacker, O. and
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Pred. No. 3.5e-120;
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/wol_type="unassigned DNA"
                                                            /product="GAGE-8"
/protein_id="AAC33676.1"
/db_xref="G1:3511023"
'mol_type="mRNA"
'db_xref="taxon:9606"
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Sequence 17 from patent
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93.8%; Score 504.8;
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JP 2002507112-A/10.
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nor rejection antigens,
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Pred. No. 4.8e-115;
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Pred. No. 4.8e-115;
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Isolated peptides derived from tumor
             organism='Homo
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Location/Qualifiers
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Sequence 17 from patent US 5648226.
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                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                        Location/Qualifiers
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98.1%;
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S bebacker, 0. Eynde, B. V. D. and Falleur, T. B.
Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, and uses thereof rejection antigen, the tumor rejection antigen, and uses thereof LUDWIG INSTITUTE FOR CANCER RESEARCH
PD 22002507112-A/10
PD 05-MAR-2002
PF 23-UN-1997 JP 1998503430
PR 24-UN-1996 US 08/66916
PI 0LIVER DEBACKER, BROIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC A61X3B/00, A61X45/05, C07X7/00, C07X14/82, C12N15/00 CC Strandedness: Single,
CC Topology: Linear;
FH Key
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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2 (bases 1 to 528)
Van Den Eynde, B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
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EPATQRQDPAAAQEGEDEGASAGQGPKPEADSQEGGHPQTGCECEDGPDGQEMDPPNP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)

    (bases 1 to 528)
    Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.

                          CTGAGATTCATCTCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
      CTGAGATTCATCTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="adult"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  Pred. No. 4.8e-115;
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Avalon Pharmaceuticals (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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ACCESSION VERSION KEYWORDS

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AUTHORS TITLE

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Eukaryotzi, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 524)

1 (bases 1 to 524)

1 (chen, M.E., Lin, S.-H., Chung, L.W.K. and Sikes, R.A.

Isolation and characterization of PAGE-1 and GAGE-7: new genes expressed in the INCaP prostate cancer progression model that share homology with melanoma associated antigens

2 (bases 1 to 524)
                                                                                                                                                                                     /trānslation="mswrgrstywprprryvoppevigpmrpegfsdevedatperg
bpatorodpaaaobgedbgasagqgpkpeadsqeqqqppgtgcecedgpdgqevdppnp
bevktpergekqsqc"
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Homo sapiens melanoma antigen related GAGE-7 mRNA, complete cds.
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                                                                                                                                                                                                                                                                                               Score 498.8; DB 9;
Pred. No. 1.5e-113;
0; Mismatches 7;
                                                                                                  /codon start=1
/product="GAGE-6 protein"
/protein_id="AAA82749.1"
/db_xref="G1:914909"
                 /cell_line="MZ2-MEL.43"
/tissue_type="melanoma"
                                                          /dev_stage="adult"
82. .435
                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                   92.7%;
98.1%;
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.1
Matches 516; Conservative
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Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 527)

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                                                                                                                                                                                                                                                                                                                                                ACCAAGGCGCTATGTACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAG
                                                                                                                                                                                            CGCCAGGGAGCTGTGAGGCAGTGCTGTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTA
                                                                                                                                                                                                                                       CTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG
                                                                                                                                                                                                                                                                               CTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
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                                                                                                                                                 CGCCAGGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTA
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                                                                                                         Gaps
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                                                              528;
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                                                              Length
                                                                                                         Indels
                                                          Score 501.4; DB 9;
Pred. No. 3.4e-114;
0; Mismatches 6;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                          93.2%;
ilarity 98.3%;
Conservative
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U19147.1 GI:914908
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                                                                                                     518;
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419

The State of the last

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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/cell line="Incar" (c4-2"
/note="isolated from prostate cancer cell lines by
differential display PCR; expression pattern correlates
with progression from androgen sensitive to androgen
insensitive in the human prostate cancer progression model
LNCaP to C4-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="melanoma antigen related GAGE-7"
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/db_xref="G1:3300090"
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BEVXTPEEGERQSQC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 ATCACAGTGTTAAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATTTTGGAAATTT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAAGTGGAACCAGCAACACCTGAAGAAGGGGGAACCAGCAACTCAACGTCAGGATCCTGC 241
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Chen,M.E., Lin,S.-H., Chung,L.W.K. and Sikes,R.A.
Direct Submission
Submitted (07-APR-1998) Urology, University of Virginia, Box 422,
Charlottesville, VA 22908, USA
Location/Qualifiers
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/note="similar to GAGE family of melanoma antigens"
/codon_start=1
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Search completed: August 8, 2004, 11:56:15 Job time : 2567 secs

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8, 2004, 12:44:49; Search time 2561 Seconds (without alignments) 9477.587 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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gp v: *
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                                                                                                                  OM nucleic - nucleic search,
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Maximum DB seq length: 560
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ARO28489 Sequence 155852 Sequence 15 155852 Sequence 15 15132468 Isolated, U19144 Human GAGE- ARO28491 Sequence 15231800 Isolated, 155854 Sequence 17 155854 Sequence 17 155854 Sequence 18 155853 Sequence 18 155853 Sequence 18 155855 Sequence 18 155857 Sequence 18 155851 Sequence 14 155851 Sequence 155851 Sequence 16 155851 Sequence 17	linear PAT 29-SEP-1999 DeBacker, O. and e tumor rejection antigen
SUMMARIES 3 ID	6 BD231798 6 BD231798 6 BD231798 6 BD231798 6 BD132468 9 HSU19144 6 AR028491 6 BD231800 6 BD231800 6 BD231800 6 BD231801 6 BD25854 6 BD025874 6 BD025874 6 BD025874 6 BD01325 6 AX284300 6 AX2865680 6 BD111325 6 AX286569	560 bp DNA US 5858689. den Eynde,B., ed from the gag
ry ch Length DB	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	15 from p 1 GI:594 i.ed. 1 to 560 suruggen, p. Peptides
% Query Score Match	444444444444444444444444444444444444	⊢ ₩
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PR 23-JAN-1998 US 09/012818
PI PIERRY BOON FALLEUR
PI THIERRY BOON FALLEUR
PC CO7K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: single,
CC TPOOLOGY: Linear;
CC TPOOLOGY: Linear
FT Rey Location/Qualifiers
FT Source Location/Qualifiers
FT Source / Organism='Homo sapiens (human)'.
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Location/Qualifiers
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llarity 100.0%; Pred. No. 7.3e-137;
Conservative 0; Mismatches 0;
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Sequence 15 from patent US 5648226.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalai, Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 560)

Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, T.B.

Isolaced polypeptides binding with HIA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof

LUDWIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapiens (human)

PN 7P 2002509859-A/8

PD 02-APR-2002
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100.0%; Pred. No. 7.3e-137;
iive 0; Mismatches 0;
         S 5858689-A 15 12-JAN-1999;
Location/Qualifiers
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/organism="unknown"
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JP 2002509859-A/8.
Homo sapiens (human)
                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 560; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
PN JP 2002507112-A/8

PD 05-MAR-2002

PP 23-JUN-1997 JP 1998503430

PR 24-JUN-1996 US 08/669161

PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR 1

A61K88/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC

Strandedness: Single;

CC Tpoology: Linear,

FH Key Location/Qualifiers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGAAGGGGAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGT
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                                                                                                                                                                                                                                                                                                                                                       CTCATATTTCACACAGATGAGTTGGCGAGGAAGATCGACCTATTATTGGTCTAGGCCAAT
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                 100.0%; Score 560; DB 6; Length 560; 100.0%; Pred. No. 7.3e-137;
                                                                                                                                                                                                                                                                                                                   Indels
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0
                                                                                                                                    Location/Qualifiers.
                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GAGE-3 protein mRNA, complete cds.
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Homo sapiens
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Debacker, O., Eynde, B.V.D. and Falleur, T.B.
Debacker, O., Eynde, B.V.D. and Falleur, T.B.
Scolated, mucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof Patent: JP 2002507112-A 8 05-MAR-2002,
LUDWIG INSTITUTE FOR CANCER RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor rejection antigen, and uses thereof.
                                                                                                                                                                                                                                                                                                                                     AATAGGTCGATCTTCCTCGCCAACTCATATTTCACACAGATGAATCTCAGTAGAGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                             GCAACTCAACGTCAGGATCCTGCTGCTGCTCAGGAGGAGGAGGATGAGGATCAGGATCTGCA
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                                                                                                                                                                                                                                Gaps
1 (bases 1 to 560)
Van den Bynde,B., DeBacker,O. and Boon-Falleur,T.
Isolated peptides derived from tumor rejection antigens, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen.
                                                                                                                                                                                                                              0
                                                                                                                                                                                             Length 560;
                                                                                                                                                                                         100.0%; Score 560; DB 6; Length 5 100.0%; Pred. No. 7.3e-137; ative 0; Mismatches 0; Indels
                                                                    Patent: US 5648226-A 15 15-JUL-1997;
Location/Qualifiers
                                                                                                                     /organism="unknown"
/wol_type="unassigned DNA"
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synthetic construct
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                AUTHORS
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KEYWORDS
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BD132468
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Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.
BD231800.1 GI:33041570
UP 200209859.A/10.
                                                                                               PAT 29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 ATGAIGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT 532
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                                                                                                                                                                                                                                                                     Boon-Falleur, T. Isolated peptides derived from the gage tumor rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 ATGATGCAGGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 532;
                                                                                                                                                                                                                                      1 (bases 1 to 532) van den Eynde, B., DeBacker, O. and van der Bruggen, P., van den Eynde, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                79.7%; Score 446.4; DB 6;
larity 99.8%; Pred. No. 7e-107;
Conservative 0; Mismatches 1;
                                                                                               DNA
                                                                                                                                                                                                                                                                                                          precursor and uses thereof
Patent: US 5858689-A 17 12-JAN-1999;
                                                                                       Sequence 17 from patent US 5858689.
AR028491.1 GI:5940464

    .532
/organism="unknown"
/mol_type="unassigned DNA"

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Homo sapiens
         541 CTGCAAAGAAA 552
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Unclassified.
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                                                                                                                                                                               Unknown.
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BD231800
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                                                                                                                                                         Submitted (28-DEC-1994) Benoit J Van Den Eynde, Ludwig Institute Submitted (28-DEC-1994) Benoit J Van Den Eynde, Ludwig Institute
                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="GABE-3 protein"
/product="GABE-3 protein"
/protein_id="MAAA2746.1"
/db_xref="G1"|4903"
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         De Backer, O., Gaugler, B., Lucas, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCA
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                       A new family of genes coding for an antigen recognized autologous cytolytic T lymphocytes on a human melanoma J. Exp. Med. 182 (3), 689-698 (1995)
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Pred. No. 9.4e-135;
0; Mismatches 0;
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                        sex="female"
cell line="MZ2-MEL.43"
                                                                                                                                                                                                                                                                                                                                     /tissue_type="melanoma"
/dev_stage="adult"
den Eynde, B., Peeters, O., Boon, T.
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100.0%; Pre
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Van Den Eynde, B.J.
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AUTHORS REFERENCE

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PN JP 2002507112-A/10

PD 05-MR-2002

PR 24-JUN-1997 JP 1998503430

PR 24-JUN-1996 US 08/669161

PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC

A61K38/00, A61K45/05, C07K7/00, C07K14/82, C12N15/00 CC
               Unclassified.

1 (Dases 1 to 532)
Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGGGAGAGGATGAGGGAG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG 384
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                                                                                                                                                                                                                                                  Length 532;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                Score 446.4; DB 6
Pred. No. 7e-107;
0; Mismatches 1
                                                                                                               Patent: US 5648226-A 17 15-JUL-1997;
                                                                                                                                                                                           /mol_type="unassigned DNA"
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                                                                                                                                     Location/Qualifiers
                                                                                                                                                   1. .532
/organism="unknown"
                                                                                                                                                                                                                                              79.7%;
99.8%;
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Best Local Similarity
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             1 (bases 1 to 532)

Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, T.B.

Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, T.B.

Isolated polypeptides binding with HIA-229 molecule, nucleic acids as molecules encoding the same, and utilization thereof Patent: JP 2002509899-A 10 02-APR-2002;

LUDWIG INSTITUTE FOR CANCER RESEARCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                     12-JAN-1999 JP 2000528586
23-JAN-1998 US 09/012818
PIERRE VAN DER BRUGGEN, BENOIT VAN DEN EYNDE, OLIVIER
                                                                                                                         OS Homo sapiens From Carlo Ressances
OS Homo sapiens From Carlo Ressances
DE 20-2APR-2002
PP 12-3AN-1999 JP 2000528586
PR 23-JAN-1999 US 09/012818
PI THERRE VAN DER BRUGGEN BENOIT VAN DEN EYNDE, OLIVIER
PC COTK4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00 CC
Strandedness: Single,
CC STRANDEDNESS:single,TOPOLOGY:linear
FR Key
Location/Qualifiers
FT Source /Organism='Homo sapiens (human)'.
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Pred. No. 7e-107;
0; Mismatches 1; Indels
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/organism="Homo sapiens"
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/db xref="taxon:9606"
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Sequence 17 from patent
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99.8%;
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PAT 18-SEP-2002

VERSION KEYWORDS SOURCE

RESULT 8

155854 LOCUS

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Score 443.2;
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De Backer, O.R.Y.
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SOURCE
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AUTHORS
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Pred. No. 4.9e-106;
0; Mismatches 3;
                                                                                                                     Score 446.4; DB 6;
Pred. No. 7e-107;
); Mismatches 1;
                         Location/Qualifiers.

    .532
    ^organism="synthetic construct"
mol_type="genomic DNA"
    /db_xref="taxon:32630"

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Location/Qualifiers
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AR275666
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De Backer,O., Van den Eynde,B.
Isolated, truncated nucleic aci
                                   Location/Qualifiers
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Strandedness: Single;
CC Topology: Linear;
FH Key I
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99.8%;
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ilarity 99.3%;
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Best Local Simi
Matches 445;
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VERSION
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TITLE
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EPATQRQDPAAAQEGEDEGASAGGGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNP
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1 (Dases 1 to 526)
De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C., Eckay, S., Viares, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van der, Eynde, B., Boon, T. and van der Bruggen, P. Chomez, P., Van de Characterization of the GAGE genes that are expressed in various
GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACACGCCTCCTGAAATGA
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                                                                                    TTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                       Treegcctatecegccceaecactreagreagreagregaaccaccaccaccreageae
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Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
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AF055474
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Cancer Res. 59 (13), 3157-3165 (1999)
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/codon_start=1

/product="GAGE-7B"

/protein_id="AAC33677.1"

/db_xref="G1:3511025"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BUZ31799 540 bp DNA linear PAT 17-JUL-2003 Isolated polypeptides binding with HLA-A29 molecule, nucleic acids BD231799
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                                                                                                                                                                          CTGGGTGTGAGTGTGAGAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 540)
Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, T.B.
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof Patent: JP 2002509859-4 9 02-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEBACKER,
                            CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCCACAGA
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                                                                                                                            CTGGGTGTGAGTGTGATGGTCCTGATGGGCAGGAGATGGACCCCGCCAAATCCAGAGG
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                                                                                                                                                                                                                                                                          393 AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
                                                                                                                                                                                                                                                                                                                           ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                         453 ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
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                                                                   273 CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
JP 2002509859-A/9
02-APR-2002
12-JAN-1999 JP 2000528586
23-JAN-1999 US 09/012818
PIERRE VAN DER BRUGGEN, BENOIT VAN DEN EYNDE, OLIVIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIERRY BOON FALLEUR
COTK4/12, CIZNI5/09, C12P21/00, C12Q1/02, C12N15/00
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Pred. No. 4.9e-106;
); Mismatches 3;
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Topology: Linear;
STRANDEDNESS:single,TOPOLOGY:linear
STRANDEDNESS: Location/Qualifiers
Location/Qualifiers
1. 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 ACAGCCTTCTGCAAAAAAAAAAAAA 540
                                                                                                                                                                                                                                                                                                                                                                                                                          533 ACAGCCTTCTGCAAAGAAAAAAAA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .540
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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JP 2002509859-A/9.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OS Homo sapiens (huma PN 72.025.09859-A/9 PN 72.04R-20.02 PF 12.04R-1999 UP 200 PR 23.04R-1999 UP 200 PR PIERRE VAN DER BRUP I THIERRY BOON FALLER PC COTK4/12, C12N15/09 Strandedness: Single; CC Topology: Linear; CT Topology: Linear; CC Top
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Best Local Similarity 99.3
Matches, 445; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGGATGAGGAGG
                                                                                                                                                                                                                                                                       Boom Falleur, T.
Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
Patent: US 5858689-A 16 12-JAN-1999,
Location/Qualifiers
                                                                                                                                                                       TIGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACTGAAGAAG
                                                                                                                                                                                                         TTGGGCCTATGCGCCCGAGCAGTTCAGTGAAGTGGAACCAGAAAGTGAAAGTAGGAAG
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Pred. No. 4.9e-106;
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  Pred. No. 4.9e-106;
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| organism="unknown"
| mol_type="unassigned DNA"
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                       Mismatches
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99.3%;
99.38;
                       Conservative
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Unclassified.
Best Local Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab.host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/note="Grgan: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; ollgo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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CDNA Library Preparation: Life Technologies, Inc.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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512 ACAGCCTTCTGCAAAGAAAAAAA 537
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                                                                                                                                                                                                                                                                                                              /done lib="SSSNU48s1"
//done lib="SSSNU48s1"
//done lib="SSSNU48s1"
//dote="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoR1;
Site_2: Not1; The poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoR1 site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was circularized with E. coli DNA ligase after digestion of EcoR1 which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof* by electroporation method. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(4T) 14 as 3' primer. The PCR products were used as template for transcription reaction when your verver including T2 promotor as 5' primer when your verver were constitution reaction when your verver including T3 promotor as 5' primer when your verver were constitution reaction when your verver constitution reaction when your verver constitution reaction when your verver transcription was a primer. The PCR products were used as template for transcription reaction when your verver constitution was a primer. The pCR products were used as template for transcription was such as a template for transcription was such as the purple was a primer constitution was such as the purple was a primer constitution was and purple was a purple was purple was a purple was purple was a 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded CDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted CDNA libraries were constructed by transformation of the remaining DNA into competent cells B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGAAGATCGACCTATTATTGGCCTAGACCCAAGGCGCTATGTACACCCTCCTGAAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 GGGAACCAGCAACTCCAACGICAGGAICCTGCAGCTGCTCAGGAGGGAGAGGAIGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gegaaccagcaacrcaacgrcaegarccrdcagcrdcrcaggaggagagagagagag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGAACACGTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 441.2; DB 12; Length 537; Pred. No. 2.6e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli Top10F' with electroporation method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                             clone="S5SNU48481-8-F10"
                                                          'organism="Homo sapiens"
                                                                                                                                                                                                                                cell_type="Epithelial"
cell_line="SNU-484"
lab_host="Top10F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGCCTTCTGCAAAGAAAAAAA 558
                                                                                                                                                                                                              tissue_type="Stomach"
                                                                                                                     xref="taxon:9606"
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                  sex="M"
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Best Local S
                                    source
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AI381509.1 GI:4194290
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /uzte="InAdg998RZ13161; INAGE:1256204"
/tissue_type="pooled germ cell tumors"
/tissue_type="pooled germ cell tumors"
/lab host="ni10B"
/clone lib="NGI GAP GG3"
/other lib="NGI GAP GG3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo (dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Seco RI sites of the modified pT7T3 vector. Library is not normalized Library was constructed by Bento Soares and M. Patima Bonaldo."
                                                                                                                                                                                                                        BX108227 S21 bp mRNA linear BST 06-FEB-2003 BX108227 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGp998K213161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
    535
                     361 ATGCAGGCTGCTCTATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTTACA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGGGCCTATGCGGCCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 TIGGGCCTATGCAGCCCGAGCTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seg primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

(Dases 1 to 521)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human Unigeneset - RZED3

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAAGATCGACCTGTTATTGGCCTAGTCCAAGACGCTATGTACAGCCTCCTGAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPOLLS I.M. AG. B. CONA Clone Collection,
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
Human UnigeneSet - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/ogi-
bin/ShowLib.pl.ogi/response7libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Fax: +49 30 32639 101

www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                \mathtt{IMAGE:}125620\overline{4}, \mathtt{mR\overline{N}A} sequence.
                                                                               GCCTTCTGCAAAGAAAAAAAAA
                                                                                                                                                                                                                                                                                                           BX108227.1 GI:27835080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPD; IMAGp998K213161.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ina Rolfs
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                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                        BX108227
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/lab hose="horserors" / Tab hose="horserors" / Tab hose="horserors" / Tab hose="longan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNZ from three normalized libraries (fetal lung NbH19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries The pools consisted of I.M. A.G.B. clones 297480-302097, 682632-687239, 756408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAG
                                                                                                                                                  CATCTGCAGGTCAAGGGCCGAAGCCTGAAGGTGATAGCCAGGAACAGGGTCACCCACAGA 352
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI381509
447 bp mRNA linear EST 28-MAR-1 te76b07.x1 Soares_NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
                                                       435 ATGATGCAGGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
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/organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:2092597"
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nx15ell.sl NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence. AA738037
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Contact: Robert Strausberg, Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M Bento Soares, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 511 Std Error: 0.00
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
tracer in a subtractive hybridization reaction. The drives PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-72811, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                      DB 10;
                                                                                                                                                                                   77.4%; Score 433.6; DB 10 199.1%; Pred. No. 1.3e-85;
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/lab host="DH108"
/clone lib="Soares NFL T GBC S1"
/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site=1: Not I; Site=2: Eco R1; Bqual amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 45:7)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                Gaps
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         Pred. No. 7.5e-86;
; Mismatches 4;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                Conservative
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/clone lib="NIH MGC 119"
/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: NotI;
/notice age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 20-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 AIGAIGCAGCTGCTCCTAIGTTGGAAAITTGTTCATTAAAATTCTCCCAAIAAAGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA
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                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MG clone distribution information can letter.//image.llnl.gov

Plate: LiAM11419 row: p column: 13

Hith: LiAM11419 row: p column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS CF780547 517 bp mRNA linear ESJ DEFINITION AGENCOURT_15739102 NIH_MGC_217 Homo sapiens CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.6%; Score 429.2; DB 12; larity 99.1%; Pred. No. 1.2e-84; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Invitrogen). Research Genethis is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/dlone="IMAGE:5168892"
/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 519.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCCTTCTGCAAAGAAAAAAA 558
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             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                .. .527
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Best Local Similarity
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             JOURNAL
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                                       COMMENT
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sapiens cDNA clone IMAGE:5168892 5',
                                                                                                                                                                                                                                                                                                                                                                                                             germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292
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                                                                                                                                                                                                                                               /tissue_type="pooled germ cell tumors"
/lab host="DH10B"
/clone_lib="NG1 CGAP_GG3"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
Polylinker; 1st strand cDNA was prepared from 3 pooled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACAACACTGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 AGGIGAAAACGCCIGAAGAAGGIGAAAGCAAICACAGIGIIAAAAGAAGGCACGIIGAA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 432; DB 9; Length 464;
Pred. No. 2.8e-85;
0; Mismatches 10; Indels
primer: -40ml3 fwd. ET from Amersham
quality sequence stop: 435.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCCTTCTGCAAAGAAAAAAA 560
                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGCCTTCTGCAAAAAAAAAAAAA 7
                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1256204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           527
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BI826605
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TITLE
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BI826605
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Gaps

322 412 382 472 442 532 502

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/clone libe "Soares testis NHT"
/note="Wector: pT7T3D-Pac" [Pharmacia] with a modified
/note="Wector: pT7T3D-Pac" [Pharmacia] with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT/T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                              AA447559 489 bp mRNA linear EST 04-JUN-1997 zw81e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636 3' similar to TR:G914905 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA 172
CTGGGTGTGAGTGTGAAGATGGTCCTGATGGCCAGAGATGGACCCGCCAAATCCAGAGG 383
                                                                                                                                                      ATGATGCAGGCTGCTATGTTGGAAATTTGTTCATTAAAATTTCTCCCAATAAAGCTTT 532
                                                                                                                                                                               444 ATGATGCAGGCTGCTGTTGTTGTTGAAAATTTGTTAAAATTTCTCCCCAATAAAGCTTT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Masch and Albert, M. Bowles, L. Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Morce, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality; sequence stop: 427.
                                                                                                             384 AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
                                                                    AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAAGAAGGCACGTTGAA
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Pred. No. 1.9e-83;
0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:782636"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA447559
AA447559.1 GI:2161229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.7%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                       ACAGCCTTCTGCA 516
                                                                                                                                                                                                                                              533 ACAGCCTTCTGCA 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG 412
                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                       National Cancer Institute / NIH
Bldg. 31 Rm.0A07 Bethesda, MD 20892
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov e column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGAGGAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGGCCTATGCGCCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 TTGGGCCTATGCGCCCGAGCAGTTCAGTGAAGAGGGAACCCAGCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                 1 (bases 1 to 517)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
         IMAGE:30524555 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 517.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 ;
                             CE780547
CE780547.1 GI:37739989
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99.3%;
                                                                                             Homo sapiens (human)
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oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW016546 418 bp mRNA linear EST 10-SEP-1999 UI-H-BIOD-abg-g-06-0-UI.81 NCI_CGAP_Sub2 Homo sapiens cDNA clone NCESE2711986 3', mRNA sequence.
                                                                                                                                                                                                                           H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                      440 GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA 381
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP inter://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                              113 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                                                                                                                                     173 TTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AGGIGAAAACGCCTGAAGAAGCTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAACCAGCAACTCAGGATCCTGCAGCTGCTCAGGAGGAAGAAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGTGTGAGTGTGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AGGIGAAAACGCCIGAAGAAGGIGAAAAGCAAICACAGIGIIAAAAGAAGGCACGIIGAA
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                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                      Indels
                                                                                                                                                                          Length
                                                                                                                                                Score 420; DB 9; Le:
Pred. No. 1.3e-82;
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                     tch 75.0%;
al Similarity 98.4%;
434; Conservative
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Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.B. Consortium/LINL at:

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA760996 1.0CGAP_GC4 Homo sapiens cDNA clone IMAGE:1257855 3 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
                                                                               232
                                                                                                                                                            GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAG 292
                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                  CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA 352
                                                                                                                                                                                                                                                                                 CTGGGTGTGAGTGTGATGGTCCTGATGGCAGGAGATGGACCCGCCAAAATCCAGAGG 140
                                   379
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTGAAAACGCCTGAAGGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT 532
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
378 TT-GGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                                                                                      /clone lib="NCI_CGAP_GC4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
                                                                      TTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled germ cell
/lab_host="DH10B"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'clone="IMAGE:1257855"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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LOCUS
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SOURCE
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VERSION

COMMENT

FEATURES

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Length 455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1751408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                AI187350.1 GI:3737988
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
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AUTHORS
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                                                                                                                                      RESULT 12
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                                                   В
        8
                                                                                                                                                    /done lib="NCI CadaP Sub2"
//note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: NCI I; Site 2: Eco Ri; The
NCI CGAP Sub2 intervation is a subtracted library derived from
BI. BI constitutes a mixture of 21 normalized or
subtracted NCI CGAP Plazaries: NCI CGAP Co4,
NCI CGAP PA22. NCI CGAP PA28, NCI CGAP Co4,
NCI CGAP EA22. NCI CGAP EA28, NCI CGAP EA212,
NCI CGAP EA22, NCI CGAP EA54, NCI CGAP EA512,
NCI CGAP EA23, NCI CGAP EA54, NCI CGAP EA512,
NCI CGAP EA23, NCI CGAP EA54, NCI CGAP EA55, 1500552-150255, NCI CGAP EA55, 1500552-150255, NCI CGAP EA54, NCI CGAP EA55, NCI CGAP EA54, NCI CGAP EA55, N
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TAG TISSUE-germ cell
TAG LISSUE-ARTC"
TAG_SEQ-AAATC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 AAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 AGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAAGTGTGAAGATGGTCCTGATGG
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                                                                                                           /clone="IMAGE:2711986"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 407.4; DB 9
Pred. No. 7.8e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.7%;
98.6%;
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Best Local Simi
Matches 411;
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Donaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gow/bbrp/image.image.html
Insert Length.504 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 391.
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Bco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Econed into the Not I and Eco RI sites of the modified pl773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                               AI187350 455 bp mRNA linear EST 10-NOV-1998 qf29a05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1751408 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 TTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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/clone lib="Scares testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 bp mRNA linear EST 16-MAR-1998 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245 to SW:GGE2_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
    TTGGGCCTATGGCCCGGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAG 218
                                                                                                                                                                                                           CATCTGCAGGTCAAGGGCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGA 338
                                                                                                                                                                                                                                                                                               CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG 398
                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 426) NCI-CSAP http://www.ncbi.nlm.nih.gov/ncicgap. Naci-CSAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGGTGTGAGTGTGTGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                             219 GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGAG
                                                                                                                                                                   CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA
                                                                                                                                                                                                                                                                                                                                                AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAA 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOLORALY Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NGT-CGAP Clone distribution
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wr
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 363.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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/db_xref="taxon:9606"
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lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA868226.1 GI:2963671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
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ak48h07.s1 S
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AA868226/c
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DEFINITION
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ORGANISM
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TITLE
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KEYWORDS
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                                                                                                                              CTGGGTGTGAGGTGTGGTCCTGATGGCAGGAGATGGACCCGCCAAATCCAGAGG 148
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CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCCACAGA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/note="Grgan: liver; Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                    CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                      CATCTGCAGGTCAAGGCCCGAAGCTCATAGCCAGGAACAGGGTCACCCACAGA
                                                                                                                                                                            AGGTGAAAACGCCTGAAGAAGGTGAAAGCAATCCCAGTGTTAAAAGAAGAACGCTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12026 row: 1 column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         533 ACAGCCTTCTGCAAAAAAAAAAAA 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
                                                                                                                                                                                                                                                                                                                                                                                                   27 ccasccrrcrscaaaaaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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1 (bases 1 to 509)
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Matches 407; Conserv
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1 (Dases I to 505)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB115693 505 bp mRNA linear EST 28-JAN-2003 K-EST0159805 L8SCKO Homo sapiens CDNA clone L8SCKO-8-B09 5', mRNA
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                                                                                                                                              130 TATTGGCCTAGACCAAGGCGCTATGTACAGCCTCTGAAGTGATTGGGCCTATGCGGCCC 189
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one round of normalization to Cot5, an
by Bento Soares and M. Fatima Bonaldo
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong-yusenong-gu, Daejeon 305-333, South Korea
Fat: +82-42-860-4470
                                                                        426;
                                                                       Length
                                                                                                          14; Indels
                                                                   Score 398.8; DB 9;
Pred. No. 6.3e-78;
0; Mismatches 14;
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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/organism="Homo sapiens"
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Plate: 8 row: B column: 09
High quality sequence stop: 505.
Location/Qualifiers
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'db_xref="taxon:9606"
'clone="L8SCK0-8-B09"
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/lab_host="Top10F'"
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/note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares Laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research colture."
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clone lib="L8SCK0"
                                                                                                                                                                                66.8%;
                                                                                                                                                                                                                      Conservative
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Job time : 2818 secs
                                                                                                                                                                                                   Similarity
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Compugen Ltd.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compus
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OM nucleic - nucleic search, using sw model

8, 2004, 12:43:29; Search time 374 Seconds (without alignments) 6360.938 Million cell updates/sec August Run on:

560 1 CTCATATTTCACACAGATGA......CTGCAAAGAAAAAAAAA 560 score: Sequence: Perfect

US-09-782-745-15

IDENTITY NUC Scoring table:

3373863 seqs, 2124099041 residues Searched:

Gapop 10.0 , Gapext 1.0

5090240 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 560 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseg 29Jan04:* Database :

geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn1980s:*
geneseqn1990s:*
geneseqn2000s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

			æ			SOFTERS	
Result No.	1t 0.	Score	Query	Length	DB	Ω	Description
	П	260	100.0	560	2	AAX90520	Aax90520 GAGE-3 t11
	7	552	98.6	560	N	AAV18718	
	m	446.4	79.7	532	~	AAX90522	_
	4		79.1	526	7	ADA15802	_
	r)	443.2	79.1	540	7	AAX90521	GAGE-
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AAS69484	ABZ18686	ABZ19551	ABZ20497	ABZ19955	ABZ19755	ABZ20480	AA160530	ABZ19533	ABZ19791	ABT15728	AAD14981	ABT15736	AAF68151	ABK38062	ACA10391	ABX99342	ADE72125	AAD24228	ABA92217	AAH93807	AAS63900
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27.8	27.0	27.0	26.8	26.8	26.8	26.7	26.3	24.5	24.5	23.6	23.0	22.1	19.3	19.3	19.3	19.3	19.3	18.5	18.5	18.1	18.1
155.4	151.4	151.4	149.8	149.8	149.8	149.4	147.4	137.4	137.4	132.2	128.8	123.8	108	108	108	108	108	103.6	103.4	101.6	101.6
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ALIGNMENTS

AAX90520 standard; cDNA; 560 BP AAX90520; RESULT 1 AAX90520

(first entry) 30-SEP-1999

GAGE-3 tumour rejection antigen clone nucleotide sequence.

Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic I lymphocyte; GAGE; ss.

Homo sapiens.

WO9937665-A1.

29-JUL-1999.

99WO~US000775. 12-JAN-1999; 98US-00012818. 23-JAN-1998; (LUDW-) LUDWIG INST CANCER RES.

Boon-Falleur T; Debacker O, Van Den Eynde B, Van Der Bruggen P,

WPI; 1999-469111/39.

tumor New isolated peptides which bind to HLA-A29 molecules, which are rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.

Example 13; Fig 4; 62pp; English.

antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (TLE) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present The present invention describes peptides which bind to human leukocyte invention

Sequence 560 BP; 177 A; 119 C; 150 G; 114 T; 0 U; 0 Other;

96US-00669161.

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                                                                                 AATAGGTCGATCTTCCTCGCCAACTCATATTTCACAGAGAAATCTCAGTAGAGAAAA
                                                                                                                     TCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCT
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                                            CTCATATTTCACACACAGATGAGTTGGCGAGGAAGATCGACCTATTATTGGTCTAGGCCAAT
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aa:Thr)
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0; Mismatches 0
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        Query Match
Best Local Similarity 100.
Matches 560; Conservative
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The present sequence encodes a GAGE-3 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal itsue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or wrine can be observed and then used to confirm a diagnosis of melanoma using cytolytic call clone proliferation methodologies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                    tumour rejection
peptides, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.6%; Score 552; DB 2; I
99.1%; Pred. No. 8.1e-149;
                                                   Boon-Falleur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. skin graft or organ transplants
                                                                                                                                                                                       Isolated nucleic acid encoding GAGE processed by HLA-CW6 molecules into
                                                                                                                                                                                                                                                                                                    Example 13; Fig 4; 60pp; English.
(LUDW-) LUDWIG INST CANCER RES
                                                   Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                      Van Den
                                                                                                         WPI; 1998-076905/07.
P-PSDB; AAW47600.
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Best Local Simi
Matches 555;
                                                      Debacker O,
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481 GGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                                                                                    Human leukocyte antigen, HLA-A29; tumour rejection antigen, detection, therapy; pathological condition; cancer; CTL; cytolytic I lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated peptides which bind to HLA-A29 molecules, which are tumor rejection antigens used for detection and therapy of pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
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                                                                                                                                                                                                       GAGB-5 tumour rejection antigen clone nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 446.4; DB 2;
Pred. No. 2.3e-118;
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0; Mismatches
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                            CTGCAAAGAAAAAAAA 560
                                                     CTGCAAAGAAAAAAAAA 560
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                                                                                                                           BP
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                                                                                                                           CDNA; 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. cancer.
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                                                                                                                          AAX90522 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Der Bruggen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                   Human leukocyte
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                   WO9937665-A1
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                                                                                                                                                     AAX90522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid molecules encode turmour rejection antigen precursors, which complex to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human leukocyte antigen; HLA; tumour rejection antigen precursor; major histocompatibility complex; MHC; cytolytic T cell proliferation; chromosome Xp11.2-p11.4.
                                            385 AGGTGAAAAGGCCTGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
CTGGGTGTGAGTGTGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                                                                     AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
                                                                                                                                                                                                                                      473 ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                                                   445 Andarideaggergerecrargradaaarrrerraaraaarrereeeaaraagerrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aa: GPMRPEQGSDEVPEMI)
aa: HPQTGKPEAHSQEQ)
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'product= "Human GAGE-7B"
                                                                                                                                                                                                                                                                                                                                                                  533 ACAGCCTTCTGCAAAAAAAAAAAA
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major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents CDNA encoding the human GAGE-7B polypeptide of the invention. The gene resides on chromosome Xpll.2-pll.4.
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Best Local Similarity 99.3%;
Matches 445; Conservative
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                                                                                                                                                     The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic Thymphorytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
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     tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>AGGTGAAAAAGCCCTGAAGAAAGGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGGGCCTATGCGGCCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treedectraridedececedadearreagrandaridaacideaacacacacacadaada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGTGTGAGTGTGATGGTCCTGATGGCCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIGGGTGTGAGTGTGAAAGATGGTCCTGATGGGCAGAAATGGACCCGCCAAATCCAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
New isolated peptides which bind to HLA-A29 molecules, which are rejection antigens used for detection and therapy of pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGE-6 tumour rejection antigen clone nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 443.2; DB 2;
Pred. No. 1.9e-117;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGCCTTCTGCAAAGAAAAAAAAA
                                                                                                              Example 13; Fig 4; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity 99.3
445; Conservative
                                                            conditions, e.g. cancer.
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Matches
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                                                                                                                                                                          The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into lumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                   172
                                                                                                                                                                                                                                                                                                                                                92 GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA 151
                                                                                                                                                                                                                                                                                                                                                                      TIGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG 232
                                                                                                                                                                                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                                                                                                                                           GGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAAGGATGAGGAGA 292
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                                                                                                                                                                                                                                                                                                                               GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGTGTGAGATGGTCCTGATGGCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGCAGGCTGCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                Boon-Falleur T;
                                                                                                                   New isolated peptides which bind to HLA-A29 molecules, which are rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.
                                                                                                                                                                                                                                                                                                                ٠<u>;</u>
                                                                                                                                                                                                                                                                                            Length 540;
                                                                                                                                                                                                                                                                   Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                Debacker O,
                                                                                                                                                                                                                                                                                          Score 441.6; DB 2;
Pred. No. 5.5e-117;
                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGCCTTCTGCAAAGAAAAAAAAA 560
                                                                              Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCCTTCTGCAAAAAAAAAAAAA
                                                                                                                                                           Example 13; Fig 4; 62pp; English.
                                                         (LUDW-) LUDWIG INST CANCER RES
                    99WO-US000775.
                                      98US-00012818.
                                                                                                                                                                                                                                                                                        sch 78.9%;
al Similarity 99.1%;
444; Conservative
                                                                                                WPI; 1999-469111/39.
                                                                             Van Der Bruggen P,
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                   12-JAN-1999;
                                      23-JAN-1998;
 29-JUL-1999
                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                113
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AAV18720 ID AAV18720 standard; cDNA; 532 XX AC AAV18720; XX DT 30-JUL-1998 (first entry)

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30-JUL-1998 (first entry)

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precursor (TRAAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAAP protein is testis. Several GAGE TRAAP have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAS for the first 112 bases. This region of GAGE-3 DNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HAA-typing assays for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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                                                               tumour; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCACAGA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid encoding GAGE tumour rejection antigen precursor processed by HLA-Cw6 molecules into peptides, useful to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGGTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 TIGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGAGCCTCCTCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a GAGE-5 tumour tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;
                                                 GAGE tumour tumour rejection antigen precursor; TRAP; tumelanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
cDNA encoding GAGE-5 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                aa:Ala)
aa:Thr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.3%; Score 438.4; DB 2;
98.7%; Pred. No. 4.6e-116;
ive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                             (pos:189. .191, (pos:192. .194,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Den Eynde B, Boon-Falleur T;
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Fig 4; 60pp; English.
                                                                                                                                                                                                                                                                                   /*tag= a
/transl_except=
/transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                          /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           WO9749417-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
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antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                                                                                                                                                          GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
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                                                                                                                                              Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                     77.1%; Score 432; DB 2; Lilarity 97.8%; Pred. No. 3.3e-114; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung cancer related gene sequence SEQ ID NO:4660
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2000US-0209531P.
2000US-0233133P.
2000US-0233617P.
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nes 438; Conserv
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18-SEP-2000; 2
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                                                       412
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                                                                                                                                                                                                                     ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT 532
            CATCTGCAGGTCAAGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid encoding GAGE tumour rejection antigen precursor processed by HLA-CW6 molecules into peptides, useful to diagnose
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                                                       CTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding GAGE-6 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGE tumour tumour rejection antigen precursor; TRAP; tu
melanoma; antigen; cytolytic T cell clone proliferation;
HLA-typing assay; ss.
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aa:Ala)
aa:Thr)
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(pos:196.
(pos:199.
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/transl_except= (
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melanomas.

412

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352 331

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20-SEP-2000; 2000US-0234009P.
20-SEP-2000; 2000US-0234334P.
20-SEP-2000; 2000US-0234509P.
22-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234957P.
25-SEP-2000; 2000US-0234923P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
27-SEP-2000; 2000US-023563P.
27-SEP-2000; 2000US-023563P.
27-SEP-2000; 2000US-023563P.
28-SEP-2000; 2000US-023563P.
28-SEP-2000; 2000US-023603P.
29-SEP-2000; 2000US-023603P.
29-SEP-2000; 2000US-023603P.
20-OCT-2000; 2000US-0237172P.
02-OCT-2000; 2000US-023723P.
02-OCT-2000; 2000US-023723P.
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2000US-0237598P.
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2000US-0245084P.
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03-OCT-2000;
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(AVAL-) AVALON PHARM

Horrigan S; Endress G, Ebner R, Carter KC, Augustus M, Weaver Z; Soppet

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 4660; 44pp; English

The present invention describes a method (MI) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent neoplastic agent. The method involves exposing cells to a chemical agent or be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 or ABL70110), or is at least 55% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has eventice activity and can be used in gene therapy. MI can be used for screening an ini-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oscophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other; Sequence

Length 528;

DB 6;

77.1%; Score 431.8;

Query Match

WPI; 2002-188264/24. PE, DR,

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                                                                                            93 GAGGAAGATCGACCTATTATTGGCCTAGGACCAAGGCGCTATGTACAGCCTCCTGAAATGA
                                                                             TIGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
                                                                                                                          CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        numan; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;
human leukocyte antigen; HLA; tumour rejection antigen precursor;
major histocompatibility complex; MHC; cytolytic T cell proliferation;
chromosome Xpl1.2-pl1.4.
                                                                                                                                                                                    CATCTGCAGGTCAAGGGCCGAAGCCTGAAAGCTGATAGCCAGGAACAGGGTCACCCACAGA
                                                                                                                                                                                                                   CTGGGTGTGAGGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCCGCCAAATCCAGAGG
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                                                                                                                                                                                                                                                                                                             ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
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                                                                                                                                                                                                                                                                                                                                    ATGATGCAGGCTGCTCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
             0;
                                113 GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCC
             Indels
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3.7e-114;
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Pred. No. 3.76
); Mismatches
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/transl_except= (pos:400.
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/product= "Human GAGE-8"
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99.5%;
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             Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GAGE-8 cDNA.
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           433;
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Human bladder cancer associated cDNA sequence SEQ ID NO:144.
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                                                                                                                                   The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents cDNA encoding the very
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                               New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 cgaagccrgaagcrgaragccaggaacagggrcacccacagacrgggrgrgagrgrgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 ATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 ATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u> AAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 430.8; DB 7;
Pred. No. 7.1e-114;
0; Mismatches 37;
                                                                                                        Claim 1; Col 7-10; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.9%;
                                                                                                                                                                                                                                                                                                                                                                             chromosome Xp11.2-p11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAAA 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
P-PSDB; ADA15778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453;
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 concode the human bladder cancer-associated proteins given in ARR4814 to ARR48242). Bladder cancer-associated proteins given in ARR4814 to ARR48242). Bladder cancer-associated proteins given in ARR4814 to ARR48242). The method can be used in antisense gene therapy and in vaccine production. The method can be used in antisense gene therapy and in vaccine production. The method can be used in screening for cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 caggaagarccrarrarracccraccaagccaagccrargracagccrccrgaagrga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCACCAACACCTGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treescerarecescescescestreageareareaacescascaaceceaecascaace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGGTGTGTGAGGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
88
Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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llarity 99.3%; Pred. No. 1.1e-113;
Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 279; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                         03-JUL-2001; 2001US-0302814P.
03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                  03-JUL-2002; 2002WO-US021338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mack DH, Aziz N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABR48213.
                                                                                                                               WO2003003906-A2
                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432;
                                                                                                                                                                                                    16-JAN-2003
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BP.

ACC51027 standard; cDNA; 527

(first entry)

12-JUN-2003

ACC51027;

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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polymucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, non-small cell contracting lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary disease, fibrosis,
                                        451
                                                                                                                                                                                                                                                                                                                                                                                                     Lung cancer-associated polynucleotide, gene, ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lession; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                           532
                                                                                                            511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynuclectide that exhibits increased or decreased
                               AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACGTTGAA
                                                                                               ATGATGCAGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTT
 AGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAA
                                                                     ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAA
                                                                                                                                                                                                                                                                                                                                                                         Lung cancer-associated polynucleotide #105,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 273; 453pp; English.
                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 2001US-0284770P.
: 2001US-0290492P.
: 2001US-0339245P.
: 2001US-0350666P.
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                                                                                                                                           ACAGCCTTCTGCAAA 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0372246P
                                                                                                                                                                                                                                                               ABX76236 standard; DNA; 527
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression in lung cancer.
                                                                                                                                                                 ACAGCCTTCTGCAAA
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13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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                                                                                                                                                                                                                                                                                                                                    02-APR-2003
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                                  392
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 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511
    polypeptides are useful
  bronchiectasis. The genes, polynuclectides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of
                                                                                                                                                          GAGGAAAATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte antigen, HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic I lymphocyte;
                                                                                                                                                                               GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGA
                                                                                                                                                                                                                                      TTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACTGAAGAAG
                                                                                                                                                                                                               TTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAG
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                                                                                                                                                                                                                                                                                                                         CATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTT
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boon-Falleur T;
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                                                                                                         Length 527;
                                                                              Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGE-2 tumour rejection antigen clone nucleotide sequence.
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Debacker O,
                                                                                                         DB 7;
                                                                                                         Score 430.2; DB 7; Pred. No. 1.1e-113;
                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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                                                                                                         76.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                   Local Similarity 99.3
hes 432; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX90519 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 ACAGCCTTCTGCAAA
The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Der Bruggen P,
 bronchiectasis.
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                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW47601
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                                                                                                                                                                                                               24-JUN-1996;
            sapiens
                                                                                                                                                                                                                                                                       Debacker O,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528
                                                                                                             The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGGAACCAGCAACTCAAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour rejection antigen precursor; TRAP; tumour; diagnosis; ntigen; cytolytic T cell clone proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                ATGGTCCTGATGGGCAGGAGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                          131 ATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AGCAGTTCAGTGATGAAGTGGAACCAGCAACACTGAAGAAGAGGGGAACCAGCAACTCAAC
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                                                                                                                                                                                                                                                                                                     Gaps
                                        ection antigens used for detection and therapy of pathological
                           isolated peptides which bind to HLA-A29 molecules, which are
                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                         Length 538;
                                                                                                                                                                                                                                             Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding GAGE-4 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                          Score 429.2; DB 2;
Pred. No. 2.1e-113;
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                      Example 13; Fig 4; 62pp; English.
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92.2%;
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                                                           conditions, e.g. cancer.
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melanoma; antigen; cy
HLA-typing assay; ss.
 WPI; 1999-469111/39.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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MARKE KAKAKA

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The present sequence encodes a GAGE-4 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is contrast the only normal tissue which expresses GAGE TRAP protein is centis. Several GAGE TRAPs have been identified (see AAV1817-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAS for the first 112 bases. This region of GAGE-3 consists of ATAP or presentation of a tumour rejection antigen. Antigens shed into blood or unine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell close proliferation methodologies. Cother uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACACCCTCCTGAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTGATAGCCAGGGAACAGGGTCACCCACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 541 BP; 158 A; 117 C; 154 G; 112 T; 0 U; 0 Other;
aa:Ala)
aa:Thr)
(pos:197. .199, (pos:200. .202,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boon-Falleur
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invention. (I) and (II) have cytostatic activity and can be used in the present therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnoshing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for immunology, microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this parent did not form part of from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                  512
                             452
                                                        531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunogenic polynuclectides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA
                                                                                                                                                                                                                                                                                                             Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen; immune response; virology; immunology; microbiology; molecular biology; recombinant DNA technology; gene; ss.
                                                    AATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTT
                                                                       AATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTT
AGGTGAAAACGCCTGAAGAAGGTGAAAGCAATCACAGTGTTAAAAGAAGGCACGTTG-A
                           AGGTGAAAACGCCTGAAGAAGGTGAAAGCAATCACAGTGTTAAAAAGAAGGCACGTTGAA
                                                                                                                                                                                                                                                                                   GAGE-2 full length cDNA sequence SEQ ID NO:2890
                                                                                                                          TACAGCCTTCTGCAAAGAAAAAAAAAA 560
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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Score 421.2; DB 7; Length 530; Pred. No. 4.2e-111; 0; Mismatches 38; Indels 0.

0; Mismatches

444; Conservative

Matches

Local Similarity

Query Match

75.2%; 92.1%;

TCTTCCTCGCCAACTCATATTTCACACAGATGAATCTCAGTAGAGGAAAATCGACCTATT 130

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	August 6, 2004, 13:03:38 ; Search time 2247 Seconds (Without alignments) 10416.216 Million cell updates/sec	US-09-782-745-16 score: 540 e: 1 CGCCAGGGAGCTGTGAGGCACTGCAAAAAAAAAA	table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	d: 3470272 seqs, 21671516995 residues	Total number of hits satisfying chosen parameters: 3992016
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 540

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		ARUZ849U Sequence RD031799 Teolated	155853 Semience 16	BD132469 Isolated.	AR028492 Sequence	BD231801 Isolated	I55855 Sequence 18	BD132471 Isolated,	AR028491 Sequence	ISS854 Semience 17	BD132470 Isolated,	AX334151 Sequence	U19145 Human GAGE-	U19146 Himan GAGE-	AF058988 Homo sapi	AR028488 Sequence	BD231797 Isolated TFFBF1 Semional 14	BD132467 Isolated,	AR275666 Sequence	AFU55474 Homo sapi	AR275665 Sequence	AF055473 Homo sapi	AX886264 Sequence	AX284300 Sequence	AX284692 Sequence	AJ318881 Homo sapi	AASZI//I Sequence	BD111325 EST and e	BT007722 Synthetic	AR416094 Sequence	BUILL64/ EST AND E BC054022 Homo sani	AX226497 Sequence	AR416095 Sequence	AY226538 Semions	BC009538 Homo sapi	AX226537 Sequence AR272357 Sequence			DNA linear PAT 29-SEP-1999			, DeBacker,O. and	age tumor reje
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Isolated peptides derived from tumor rejection antigens, and their
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/organism='Homo sapiens (human)'.
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iive 0; Mismatches 0;
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/organism="unknown"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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CC Topology: Linear;
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 540)

1 (bases 1 to 540)

1 (bases 1 to 540)

2 Eruggen, P.V.D., Eynde, B.V.D., Debacker, C. and Falleur, T.B.

1 solated polypeptides binding with HiA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.

2 Extent: JP 2002508859-A 9 02-APR-2002;

2 Hown sapiens (human)

PN JP 2005509859-A/9

PD 02-APR-2002

PF 12-APN-1998 US 09/012818

PI THIERRY BOON FALLEUR
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Best Local Similarity 100.0%; Pred. No. 2.8e-129;
Matches 540; Conservative 0; Mismatches 0;
          Patent: US 5858689-A 16 12-JAN-1999;
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1 (bases 1 to 539)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and
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Pred. No. 2.8e-129;
0; Mismatches 0;
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AR028492.1 GI:5940465
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      /mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="unknown"
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R 24-JUN-1996 US 08/669161
PI OLIVIER DEBACKER, BENOIT VAN DEN EXNDE, THIERRY BOON FALLEUR PC A61X38/00, A61X45/05, CO7K7/00, CO7K14/82, C12N15/00 CC Strandedness: Single;
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Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof Patent: JP 2002507112-A 9 05-MAR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
                                                                                                                           CTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
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'mol_type="unassigned DNA"
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DN JP 2002509859-A/11

PN JP 2002509859-A/11

PD 02-APR-2002

PF 12-JAN-1999 UP 2000528586

PR 23-JAN-1999 UP 2000528586

PI THIERRY BOON FALLBUR

PC COTK4/12, C12N15/09, C12P21/00, C12Q1/02, C12N15/00 CC

Strandedness: Single,
CC Topology: Linear;
CC Topology: Linear;
CC STRANDEDNESS:single, TOPOLOGY:linear
FH Key Location/Qualifiers
FT source /organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD231801 539 bp DNA linear PAT 17-JUL-2003 Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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Van den Bynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and
                               Gaps
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 Score 534.2; DB 6;
Pred. No. 8.9e-128;
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 18 from patent US 5648226.
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Isolated peptides derived from the gage tumor rejection antigen
                                                                                         121 CCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGT
                          TGAGATTCATCTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA
                                                                                                                            GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
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van der_Bruggen,P., van den Eynde,B., DeBacker,O. and
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Pred. No. 2.2e-126;
); Mismatches 2;
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Patent: US 5858689-A 17 12-JAN-1999;
Location/Qualifiers
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/mol_type="unassigned DNA"
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1 (bases 1 to 539)

Debacker, O., Eynde, B.V.D. and Falleur, T.B.

Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof baten: JP 2002507112-A 11 05-MAR-2002;

FN JP 2002507112-A/11

PD 05-MAR-2002

PR 23-JUN-1997 JP 1998503430

PR 23-JUN-1996 US 08/669161

PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR P
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                                   CCAAGGCGCTATGTACAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCGAGCAGTTCAGT
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PR 24-JUN-1996 US 08/669161
PR 01-VUTER DEBACKER, BENOIT VAN DEN EXNDE, THIERRY
A61K38/00,A61K45/05,C07K7/00,C07K14/82,C12N15/00 C
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Pred. No. 8.9e-128;
0; Mismatches 3;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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JP 2002507112-A/11.
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QY 129 GCTATGTACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG 188 Db 121 GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180 QY 189 TGGAACCACACACCTGAAGAGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG 240 Db 181 TGGAACCAGCAACACCTGAAGAGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG 240 QY 249 CTCAGGAGGGAACACCTGAAGAGGGAACTCTGAGGACCTGAAGCTGAACTGATA 308 Db 241 CTCAGGAGGAAGAGGATGAGGAGCATCTGCAGGACCAGACCTGAACTGATA 308 QY 249 CTCAGGAGGAAGAGGAGGACTCTGCAGGACTCAAGGCCGAAGCCTGAACTGATA 308 QY 309 GCCAGGAACAGGATCACCCACAGCTCTGAGGGAGCTCAAGACCTGAACCTGATGAGCAGTA 308 QY 309 GCCAGGAACAGGTCACCCCACAGACTGGGTGAAGATGATCATCTGAAGACCTGAACAGCATCAC 428 QY 369 AGATGGACCCCCCACAGACTGGGTGAAAACGTGAAAAGGTGAAAAGCAATCAC 428 QY 369 AGATGGACCCCCCACAATCCAGACTGGAACTGGAAAGGTGAAAAGGAACTCACCCTGATGGACAATCACC 420 QY 369 AGATGGACCCCCCAAATCAAGACGGGAGGTGAAAAAGGAAAGGTGAAAAAGAAATTGTTCA 420 QY 429 AGTGTTAAAAATCCCGACACTTGAAATGATGCCCTCTATGTTGGAAATTGTTCA 420 QY 429 AGTGTTAAAAATCCCCACAATGAAGGGCTGCTCCTATGTTGGAAATTGTTCAC 420 QY 429 TTAAAAATTCTCCCAATTAAAACTTTTACAGGCTCCTCTTTGTTGGAAAATTGTTCACAATGATCACCTGTTTTTTTT	RESULT 11 155854 LOCUS LOCUS LOCUS LOCUS LOCUS Sequence 17 from patent US 5648226. ACCESSION SEQUENCE 17 RESTOR VERSION SEQUENCE OURCH NICHON. ORGANISM Unclassified. REFERENCE AUTHORS Van den Eynde, B., DeBacker, O. and Boon-Falleur, T. TITLE ISOlated peptides derived from tumor rejection antigens, and their Use JOURNAL Patent: US 5648226-A 17 15-JUL-1997; FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers ORIGIN ORIGIN	Query Match 97.9%; Score 528.8; DB 6; Length 532; Best Local Similarity 99.6%; Pred. No. 2.2e-126; Andels 0; Gaps 0; Agarchise 530; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Agarchise Gardagardaracagarchise Garchise Garchise Gardagarchise Gardagarchise Gardagarchise Gardagarchise Garchise Gardagarchise G
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Db 241 CTCAGGAGGAGGATGAGGGACATCTGCAGGTCAAGGGCCGAAGCTGAAGCTGATA 300 Qy 309 GCCAGGAACAGGGTCACCCACAGACTGGAGGTGAAGATGGTCCTGATGGCAGG 368	Cellomos 3, G	Moi_type="unassigned DNA"
QY 309 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAAGATGGTCCTGATGGGCAGG 368 Db 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAAGATGGTCCTGATGGGCAGG 360 QY 369 AGATGGACCCGCAAATCCAGAGGTGAAAACGTGAAGAAGATGACAACACACAC	RESULT 12 BD132470 LOGUS DEFINITION ISOLated, nucleic acid molecules which code for GAGE tumor ACCESSION VERSION BD132470. BD1	PEATURES CC Topology: Linear; FEATURES CC Topology: Linear; FFH Key Location/Qualifiers CC Topology: Linear; FFH Key Location/Qualifiers 1.332 CORRESTANT CONSTRUCT And_type="genomic DNA" Adb_xref="taxon:32630" ORIGIN Query Match Query Match

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2 (bases 1 to 527)
Van Den Eynde,B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
1. .527
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181 TGATGAAGTGGAACCAGCAACAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCC 240
                                                        AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGTGAAGATGGTCCTGA 360
                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Howo.
1 (bases 1 to 527)
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Pred. No. 1.2e-124;
0; Mismatches 3;
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db xref="taxon:9606"

sex="female"

/cell_line="MZ2-MBL.43"

tissue_type="melanoma"

dev_stage="adult"

82. .435
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Best Local Similarity 99.4%;
Matches 524; Conservative (
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Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
1. 528
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1 (bases 1 to 528)
2 And den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S.
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100.0%; Pred. No. 3.6e-126;
live 0; Mismatches 0;
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83. .436
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Homo sapiens
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                                                                                                                                               Description
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Contact: Kim YS Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnolog 52 Eceun-domy Vuscong-gu, Daejeon 305-333, South Kore Fax: +82-42-860-4470 Fax: +82-42-860-4470 Email: Yongsungemail. kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.		EF	TLE	21C	Front:	ier Kore	an E	Project	0		
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				Hig	h quali	ity sequ	ence	•			

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full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                BIRZE605
603077056F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5168892 5',
mRNA sequence.
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421 CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTGCTGTTGTTGGAAAT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="medulla"
/lab_host="DH10B"
/clome_lib="WHH MGC"
/note="Organ: brain; Vector: pCMV-SFORT6; Site_1: NotI;
/note="Organ: brain; Vector: pCMV-SFORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla fro
anonymous male age 27. library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTGTGTGAAATATGAGTTGGCGAGGAACGATCGACTATTTTTGGCCTAGACCAAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NH-MGC http://mgc.nci.nih.gov/.
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Email: cgapbs-r@mail.nih.gov
Tissue procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MG clone distribution information can letter through the I.M.A.G.E. Consortium/LIML at:

http://image.llnl.gov

Plate: LiAM1419 row: p column: 13
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Pred. No. 3.3e-95;
0; Mismatches 8;
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this is a NIH MGC Library."
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Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 98.5%;
Matches 519; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                    /Globe 1110=755NUAGESTS. / Calone 1110=75NUAGESTS. / Calone 1110=75NUAGESTS. / Calone 1110=75NUAGESTS. / Calone 1110=75NUAGESTS. / Calone 2: Not1; The poly (A) + RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with Tabacco including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was circularized with R. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF by electroporation method. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5 'primer and N(dT) 14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                           cell type="Epithelial"
cell_line="SNU-484"
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                                                                                                                                                                                                   tissue_type="Stomach"
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                             241 CAGGAGGGAGGATGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTCATAGC 300
                                                               CAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAG 370
                                                                                     371 ATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAG 430
                                                                                                                                                          361 ATGGACCCGCCAAATCCAGAGGAGGTGAAAAGGCTGAAGAAGATGAAAGCAATCACAG 420
                                                                                                                                                                                                TGTTAAAAGAAGCACGTTGAAAIGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATT 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BX108227 NCI CGAP GC3 Homo sapiens cDNA clone IMAGp998K213161 ; IMAGE:1256204, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Partsch, E., Peters, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RZPD; IMAGPO99RX131161.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi.
bin/showLib.pl.cgi/response?libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Radelof, U., Schneider, D. and Korn, B.
Human UnigensSet - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung (Im Neuchheimer Feld 580, D-69120 Heidelberg, Germany
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/db_xref="taxon:9606"
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CF780547
AGENCOURT 15739102 NIH MGC_217 Homo sapiens cDNA clone
IMAGE:30524555 5', mRNA sequence.
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Contact: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Genomics
National Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: capabs-remail.inih.gov.
Tissue Procurement: James Martin, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LALL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:
http://image.llnl.gov
Rligh quality sequence stop: 517.
High quality sequence stop: 517.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                    0;
         DB 13; Length 521;
                                                                    Indels
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Score 513.6; DB 13
Pred. No. 4.4e-95;
0; Mismatches 4;
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   Query Match
Best Local Similarity 99.2%;
Matches 516; Conservative
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Euteleostomi;

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/clome="Index:5402663"
/tissue_type="adenocarcinoma, cell line"
/lab_host="PH10B [phage-resistant)"
/clome_lib="NIH MGC 90"
/note="Corpan: ITver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Clomed unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clomes and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12026 row: 1 column: 24
High quality sequence stop: 509.
Location/Qualifiers
1. .509
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                                                                                   Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleoston Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 509)

NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: ogapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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                                                                                                                                         /tissue_type="Pooled Chondrosarcoma Tumor cells"
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/note="Vector: pix.Asc; Pix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CCTCGTGCCG)3. 3' Linker sequence - GCGGCGCTGAGAGCC T18. Sequencing primers 3'end: T3 promoter primer 5'd (ATTAACCCTCACTAAAGGGA)3', 5' End: T7 promoter primer 5'd (TAATACGACTCACTAGGG)3', Average insert size 0.5-1kb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ACCAGCAACACCTGAAGAAGGAGCAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 GGAGGGAGGATGAGGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTCATAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 GGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 508.2; DB 14; Length 517; Pred. No. 5.7e-94; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516
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                         'organism="Homo sapiens"
|mol_type="mRNA"
|db_xref="taxon:9606"
                                                                                                               'clone="IMAGE:30524555"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI868671
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99.4%;
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/lab_host="DH108"
/clone lib="Soares NRL T GBC S1"
/clone lib="Soares NRL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW510753 457 bp mRNA linear BST 03-MAR-2000 hd39d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. ;
                                                                                                                 342 AGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAA 401
                                                                                                                                                                                                                                                                                   CGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAG 461
       CAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGAGGAGGAGGAGCATCTGCAG 251
                                                                                                                                                                                                                                                                                                                                                                                GCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTC 521
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                     130 CGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                             70 GCTGCTCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTC
                                                                                  GTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTG
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:2911881"
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Unpublished (1997)
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/clone_lib="Soares testis_NHT"
/clone_lib="Soares testis_NHT"
/nto="Vector: pI7T3D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not 1; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                  Soares testis_NHT Homo sapiens cDNA clone IMAGE:782636 to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGACTCTTTTCCTCTACTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAGAT 101
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                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
I (bases 1 to 48)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Mhite,Y., Wylie,T., Waterston,R. and Wilson,R. Theising,B., WashJ-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41n13 fvd. ET from Amersham High quality sequence stop: 427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 473.2; DB 9; Length 489;
Pred. No. 8.4e-87;
0; Mismatches 3; Indels 1
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/db_xref="taxon:9606"
/clone="IMAGE:782636"
Location/Qualifiers
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al Similarity 99.2%;
486; Conservative
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EST 28-MAR-1999
                  germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
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te76b07.xl Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
polylinker; 1st strand cDNA was prepared from 3 pooled
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0
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                                                                                                                                                                                                                          82.7%; Score 446.8; DB 9; Length larity 98.5%; Pred. No. 2.1e-81; Conservative 0; Mismatches 7; Indels
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Seg primer: -40UP from Gibco.
Location/Qualifiers
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AI381509.1 GI:4194290
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Unpublished (1997)
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/Linn at:
www-bio.llnl.gov/bbry/image/image.html
Insert Length: 511 Std Error: 0.00
Seq primer: -40ml3 Hwd. BT from Amersham
High quality sequence stop; 435.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA/38037 464 bp mRNA linear EST 22-JAN-1998 nx15ell.sl NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1256204 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN.;, mRNA sequence. AA738037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435
                                                                                                                            ACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACC 338
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                                                                                                                                                                                                                                 AGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCCAGGATCCTGCAGGTGCTCAGGA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAAT 495
                                 GTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGT 398
                                                                                                     ACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACC 195
                                                                                                                                                                                                                                                                                                     GGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGA 315
                                                                                                                                                                                                                                                                                                                                                                                                     316 ACAGGGTCACCCACACAGACTGGGTGTGAAGATGTGATGGTCCTGATGGGCAGAGATGGA 375
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue type="pooled germ cell tumors"
/lab_host="wooled germ cell tumors"
/lab_host="wooled germ cell tumors"
/lab_host="Gap germ cell tumors"
/note="Wector: pT/T3D-Pac (Pharmacia) with a modified
  GTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGGCCGAAGGCGCTATGT
                                                                                                                                                                                                     AGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1997)
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CB115693 505 bp mRNA linear EST 28-JAN-2003
K-EST0159805 L8SCKO Homo sapiens cDNA clone L8SCKO-8-B09 5', mRNA
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                                                                                                                                                                                                                                                                                                                                     /tissue type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/close lib="NIH MGC 90"
/note="Organ: liver; Vector: pCWV-SPORT6; Site 1: Not1;
Site 2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AACCAGCAACTCAACGTCAGGATCCTGCTGCTCCAGGAGGAGGAGGATGAGGGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTG
                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANLOGS row, column: 07
High quality sequence stop: 480.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 81.2%; Score 438.6; DB al Similarity 99.1%; Pred. No. 1e-79; 441; Conservative 0; Mismatches
                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4451958"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smail: cgapbs-r@mail.nih.gov
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                              Pissue Procurement: ATCC
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                                                                         /clone_libe="Soares NFL T GBC_S1"
/clone_libe="Soares NFL T GBC_S1"
/clone_morgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Bcc RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL)9W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-3020997, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.
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I (bases 1 to 480)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.9e-80;
0; Mismatches 3; Indels 0
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L_type="mRNA"
_xref="taxon:9606"
                                                          /lab_host="DH10B"
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99.3%;
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Matches 444; Conservative
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/colne=lib="LaSCKO"
/note="Organ lib="Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
culture."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases I to 501). Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R. Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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                                                                                                                                              Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
For E Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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Unpublished (2002)
Contact: Kim YS
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/organism="Homo sapiens"
                                                                                                                                                                                                             Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 8 row: B column: 09
High quality sequence stop: 505.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="L8SCK0-8-B09"
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RESULT 12

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Trissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Trissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NOT-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.lnh.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 331.
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/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="DH10B"
/lab_host="NH10B"
/lab_host
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I (bases 1 to 450)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 2.8e-78;
0; Mismatches 5; Indels 1;
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/db_xref="taxon:9606"
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/lab host="DH10B [Life Technologies)"
/lab host="DH10B [Life Technologies)"
/clone lib="NCI CGAP Sub2"
/clone lib="NCI CGAP Sub2"
/note="Technologies"
/note="Technologies"
/not CGAP_Sub2 library is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI CGAP libraries: NCI CGAP CO4,
NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP Ed12,
NCI CGAP Ed15, NCI CGAP Ed28, NCI CGAP Ed12,
NCI CGAP Ed3, NCI CGAP Ed28, NCI CGAP Ed12,
NCI CGAP Ed2, NCI CGAP Ed58, NCI CGAP Ed12,
NCI CGAP Ed2, NCI CGAP Ed58, NCI CGAP Ed12,
NCI CGAP Ed2, NCI CGAP Ed58, NCI CGAP Ed12,
NCI CGAP Ed2, NCI CGAP Ed58, NCI CGAP Ed12,
NCI CGAP Ed28, NCI CGAP Ed28, NCI CGAP Ed12,
NCI CGAP Ed28, NCI CGAP Ed28, NCI CGAP Ed12,
NCI CGAP Ed28, NCI CGAP Ed28, NCI CGAP Ed12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the IM.A.G.E. Consortium/ILINL at:
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
               397 CCIGAAAIGAIIGGGCCIAIGCGGCCCGAGCAGIICAGIGAAGIGGAACCAGCAACA 338
                                                                         262
                                                                                                                                                                                                                       218
                                                                                                                                                                                                                                                          323 CACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGGCA 382
                                                                                                                                                                                                                                                                                                        217 CACCCACAGACTGGGTGTGTGTGTGAGTGGTCCTGATGGGCAGGAGATGGACCCGCCA 158
                                                                                                                                                               GATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGT 322
                                                                                                                                                                                                                                                                                                                                                           383 AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 GCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCA 502
                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 ACACGITGAAIGAIGCAGGCIGCICCIAIGIIGGAAAITIGIICATIAAAITICICCA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
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UI-H-BIOD-abg-g-06-0-UI.81 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711986 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                       337 CCTGAAGAAGGGGAACCAGCAACTCAACGTCCAGGATCCTGCAGCTGCTCAGGAGGAGAG
                                                                                                                                                                                                          277 GATGAGGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                        CCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2711986"
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KEYWORDS
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
www-bio.llni.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00

Beg primer: -40UP from Gibco
High quality sequence stop: 391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
/clone lib="Soares testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                  Soares testis NHT Homo sapiens cDNA clone IMAGE:1751408 to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA
                                                GCACGIIGAAAIGAIGCAGGCIGCICCIAIGIIGGAAAIITGIICAIIAAAAIICICCCA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                90 ACACGITGAAATGAIGCAGGCTGCTCCTAIGTTGGAAATTTGTTCATTAAAATTCTCCCA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398
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150 AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGAAATGATTGGGCCTATGCGGCCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGTTGGCGAGGAGGATGACCTTATTATTGGCCTAGA-CAAGGCGCTATGT-CAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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Pred. No. 6e-76;
0; Mismatches 8; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                ATAAAGCTTTACAGCCTTCTGCAAAAAAA 533
                                                                                                                                                                                                ATAAAG-TTTACAGCCTTCTGCAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'mol type="mRNA"
'db xref="taxon:9606"
'clone="IMAGE:1751408"
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97.8%;
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Homo sapiens
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Unpublished (1997)
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3' similar
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FEATURES

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TITLE

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Enzis.

These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 [IMAGE CloneIDS 1322376-132391], 14756008-1456775, 1500552-1502855)

NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 376-3778 (IMAGE CloneIDS 1323912-132891, 1471368-1472993, 1492104-1493255) NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDS 1414920-1417991, 1520904-152259) NCI CGAP GC4 pool 1 LLAM 3575-3582, 376-3720, 3733-3735, 376-759, 3062-3068 (IMAGE CloneIDS 14169064-1470993, 1475592-1476743) NCI CGAP GC4 pool 1 LLAM 3576-35631, 1469064-1470993, 1475592-1476743) NCI CGAP GC4 pool 1 LLAM 3660-36631, 16A064-1470993, 1475592-1476743) NCI CGAP CCI pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 16A064-161061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants Subtraction was performed as previously described Renald, Lennon & Soares (1996): Normalization and decombinants of the composition of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 bp mRNA linear EST 16-MAR-1998 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409245 to SW:GGE2_HUWAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
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TAG TISSUB-germ cell
TAG LISSUB-ICI CGAP GC4
TAG_SEQ=AAATC"
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGCGCTATGTACAGCCTCCTCAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGA
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Bonaldo, Ph.D. cDN trayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. close Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NGI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="DH10B"
/clone lib="Soares testis NHT"
/clone lib="Soares testis NHT"
/note="Vector: pT73D-per
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDI
was prepared from mRNA obtained_from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 TAIGITGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 TATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGNANTTGCCTATGCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGAGGGGAACCAGCAACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 GAGCAGTICAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGGAGGGAACCAGCAACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTCAGGATCCTGCAGCTGCTCAGGAGGGAGGATGAGGGAGCATCTGCAGGTCAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA
                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 426;
                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.4%; Score 402; DB 9; 97.1%; Pred. No. 3.2e-72; iive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1409245"
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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Search completed: August 6, 2004, 18:20:17 Job time: 2420 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 6, 2004, 13:00:38; Search time 329 Seconds (without alignments) 6972.726 Million cell updates/sec

Run on:

US-09-782-745-16 540 score:

Title: Perfect

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5025714 Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

seg length: 0 seg length: 540 DB DB Maximum Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N_Geneseq_29Jan04:* Database

geneseqn2000s:*
geneseqn2001as:*
geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:*
geneseqn2003cs:* geneseqn1980s:* geneseqn1990s:* geneseqn2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

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ABT15737	ABZ19533	ABX77605	ACD42232	ADC24646	AA160530	ABZ19538	AAS69484	ABT15728	AAD14981	ABT15736	AAF68151	00000000	ABA38062	ACA10391	Æ) ADE72125	AAD24228	ABA92217	AAH93807	A2563900	A MICO COLOR	7/07/17/2	AAH85121
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210	205.6	202.4	202.4	202.4	. 187	180.6	164.2	141.6	131.6	126.6	109.6	109 6	001	100	109.6	109.6	105.2	105	103.2	103.2	103.2		103.2
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ALIGNMENTS

AAX90521 standard; cDNA; 540 BP. (first entry) 30-SEP-1999 AAX90521; RESULT 1 AAX90521

GAGE-4 tumour rejection antigen clone nucleotide sequence.

Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic I lymphocyte; GAGE; ss.

sapiens. Homo

WO9937665-A1.

29-JUL-1999.

99WO-US000775. 12-JAN-1999;

98US-00012818. 23-JAN-1998;

(LUDW-) LUDWIG INST CANCER RES.

Boon-Falleur T; Debacker O, Van Den Eynde B, Van Der Bruggen P,

WPI; 1999-469111/39.

tumor New isolated peptides which bind to HLA-A29 molecules, which are trejection antigens used for detection and therapy of pathological conditions, e.g. cancer.

Example 13; Fig 4; 62pp; English.

The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present

Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 U; 0 Other;

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Gaps

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Indels

Length 540;

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The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) mclecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic Tlymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be use for stimulating CTLs in vivo. The present sequence represents a GAGB tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection
therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
GAGE; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rejection antigen clone nucleotide sequence.
                                                                                                                                                                                                                             Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                               Score 534.2; DB 2;
Pred. No. 7.7e-143;
0; Mismatches 3;
                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
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                                                    4; 62pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection;
                                                                                                                                                                                                                                                                                                                                                                               TGCAGCTGCTCAGGAGGGAGGATGAGGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGA
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                                                                                                                                                        CTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
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                                                             Gaps
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                            Length 540
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                                                             Indels
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                           ; Score 540; DB 2; I
; Pred. No. 1.7e-144;
0; Mismatches 0;
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                                            ilarity 100.0%;
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nes 540; Conserv
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540

detection;

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The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into lumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
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                                                                                                                                                                                                                New isolated peptides which bind to HLA-A29 molecules, which are rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 2; Length 532;
.7e-141;
es 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;
                                                                                                                                                      Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 528.8; I
Pred. No. 2.7e-
0; Mismatches
                                                                                                                                                        В,
                                                                                                                                                      Van Den Eynde
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                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
                                                             99WO-US000775
                                                                                          98US-00012818
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                                                                                                                                                                                   WPI; 1999-469111/39
                                                                                                                                                      Van Der Bruggen P,
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WO9937665-A1
                                                           12-JAN-1999;
                                                                                          23-JAN-1998;
                              29-JUL-1999
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Human, cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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          ABL66323 standard; DNA; 528
                                               entry)
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Weaver Z;
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Soppet DR,
                           ABL66323;
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The present invention describes a method (M1) for screening for an antinopolastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AB161664 to AB170110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an
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                                                                                                                                                                                                                                                                                                 anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M., and the data is sufficient to convey the chemical structure and/or properties of the agent. M. can be used in the treatment of cancer such
                                                                                                                                                                                                                                                                                                                                                                                          faction, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carctinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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nnt to be tested for anti-neoplastic activity, and determining a change expression of a gene of a signature gene set.
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                                                                       Claim 1; SEQ ID NO 4660; 44pp; English
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Matches 528;
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The present sequence encodes a GAGE-6 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal itsue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAP sequence. The rest of cated a position, with the exception of GAGE-3 whose 5 end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 conditions and sequence of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants
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                                           TRAP; tumour; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid encoding GAGE tumour rejection antigen precursor processed by HLA-CW6 molecules into peptides, useful to diagnose
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                                             GAGE tumour tumour rejection antigen precursor; TRAP; tu
melanoma; antigen; cytolytic T cell clone proliferation;
                                                                                                                                                                                                  aa:Arg)
aa:Ala)
aa:Thr)
               encoding GAGE-6 tumour rejection antigen precursor.
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                                                                                                                                                  Location/Qualifiers
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                                                                                HLA-typing assay; ss.
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TTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA

ВР

AAV18721 standard; cDNA; 539

RESULT 5 AAV18721 (first entry)

30-JUL-1998

AAV18721;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynuchocitide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is
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                                                                                                                                                                                                                             Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynucleotide or antibody.
                                               GCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA
                                 GCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA
                                                                                                                    GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAG
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                                                                                                                                                              CAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
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           GATGAAGTGGAACCAGAGCCTCCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
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                                                                                             GCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGATGTGAAGATGGTCTGAT
ss.
                                                                                                                                                                                                                                                                                                                                                                     Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                               Human bladder cancer associated cDNA sequence SEQ ID NO:144.
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2001US-0343705P.
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B; ABR48213.
                                                                                                                                                                                                                                                                                 standard;
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08-NOV-2001;
13-NOV-2001;
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useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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                                                                                                                                                                     Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
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                                                                                                                                                                                                                       522.2; DB 7;
No. 2.1e-139;
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                                                                                                                                                                                                                          Score Pred. 1
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                                                                                                                                                                                                                          96.78;
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                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.4
Matches 524; Conservative
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                                                                                                                                                                                                                                                                                                    The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynuclectide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynuclectides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to creat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung cancer or other benign or precamerous lesions, e.g. arelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
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                                                                                                                                                                                                   Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 522.2; DB 7;
Pred. No. 2.1e-139;
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                                                                                                                                                                                                                                                                           Claim 22; Page 273; 453pp; English.
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18-APR-2001; 2001US-0284770P.
10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC.
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99.4%;
                                                                                                                                                                                                                                                expression in lung cancer.
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                                                                                                                                                         WPI; 2003-093161/08.
P-PSDB; ABU56512.
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Best Local Similarity
                                                                                                                               Murray R;
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The present sequence encodes a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for,
361 GGGCAGGAGGTGGACCCGCCAAATCCAGAGGTGAAAACGCCTGAAGAAGGTGAAAAG 420
                                                                         481
                                                                                                                                                480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
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                                                                         CAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
                                                                                                                                        421 CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGATGCGGGCTGCTCTATGTTGGAAAT
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                                                                                                                                                                                                               TIGITCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding GAGE-5 tumour rejection antigen precursor.
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(pos:192.
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/transl_except=
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                                                                                                                                                            TGGAACCAGCAACACTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
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                                                    CTACTGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection;
therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
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                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                New isolated peptides which bind to HLA-A29 molecules, which are rejection antigens used for detection and therapy of pathological
                         0;
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     532;
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      Length
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                       Indels
 Score 520.8; DB 2;
Pred. No. 5.3e-139;
0; Mismatches 7;
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The present invention describes peptides which bind to human leukocyte antigen (HiA, A29 (HiA-A29) molecules. The peptides are processed into tumour rejection artigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HIA-typing assays. Complexes of HIA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;
human leukocyte antigen; HLA; tumour rejection antigen precursor;
major histocompatibility complex; MHC; cytolytic T cell proliferation;
chromosome Xp11.2-p11.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGA
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                                                                                                                               rejection antigen clone, from an example from the present
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                                                                                                                                                                                                     538;
                                                                                                                                                                                                                                                   CGCCAGGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCT
                                                                                                                                                                    Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                     Length
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                                                                                                                                                                                               Score 512.8; DB 2;
Pred. No. 1.1e-136;
0; Mismatches 7;
                           Fig 4; 62pp; English.
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98.1%;
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  e.g.
                          Example 13;
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conditions,
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AB017575 to AB020506 represent isolated polynucleotide (I) sequences, and ABP5446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They an also be useful in virology, incrobiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA
                                                                                                    GAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen; immune response; virology; immunology; microbiology; molecular biology; recombinant DNA technology; gene; ss.
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                                                                               449 TGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                          GAGE-2 full length cDNA sequence SEQ ID NO:2890.
                                                                                                                                                                  540
                                                                                                                                                                                                        481 CTTTACAGCCTTCTGCAAAGAAAAAAAA 512
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Pred. No. 2.16
                                                                                                                                                                  CTTTACAGCCTTCTGCAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2890; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaiger A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001US-0280255P.
28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bangur CS,
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Best Local Similarity 98.1%;
Matches 522; Conservative
                                                                                                                                                                                                                                                                                                            ABZ20463 standard; cDNA; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2002; 2002WO-US010421.
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising that encodes a human leakecyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 mucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents CDNA proliferation of cytolytic T cells. This sequence represents CDNA on chromosome Xp11.2-p11.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
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Pred. No. 1.5e-135;
0; Mismatches 2;
                                                                                                 /rransl_except= (pos:115. .162, /transl_except= (pos:265. .306,
                                                                                                                                                                                                                                                                                                                                                              Boon-Falleur T;
                                                                                 "Human GAGE-7B"
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Col 9-10; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                                                                               30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numman; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL; human leukocyte antigen; HLA; tumour rejection antigen precursor; major histocompatibility complex; MHC; cytolytic T cell proliferation; chromosome Xpl1.2-pl1.4.
                                          CTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG
                                                                                                                                     TGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCC
                                                                                                                                                                                                                                      TGGGCAGGAGATGGCCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAA
                                                                                                                                                                                                                                                                                                                                    GCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGATGCAGGCTGCTCCTATGTTGGAAA
                                                                     ACCAAGGCGCTATGTACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAG
                                                                                         Accaagacgcracgragagccrccrgaaargarraggccrargcggcccgagcagrrcag
                                                                                                                  TGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCC
                                                                                                                                                                  TGCAGCTGCTCAGGAGGGAGAGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGA
                                                                                                                                                                                      TGCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGA
                                                                                                                                                                                                                 AGCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAAGATGGTCCTGA
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                                                                                                                                                                                                                                                                                                              GCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAA
                      CTGAGATTCATCTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
CGCCAGGGAGCTGTGAGGCAGTGCTGTGTGTTTCCTGCCGTCCGGACTCTTTTTCCTCTA
                                                                                                                                                                                                                                                                                                                                                             TITGITCATIAAAATICICCCAAIAAAGCTITACAGCCTTCTGCAAAAAAA 532
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/transl_except= (pos:400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Human GAGE-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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P-PSDB; ADA15778.
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The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid molecule and the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human nuclecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents cDNA encoding the human GAGE-8 polypeptide of the invention. The gene resides on chromosome Xp11.2-p11.4.
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      New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
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                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 504.4; DB 7;
Pred. No. 2.7e-134;
0; Mismatches 6;
                                                                      English.
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                                                                                                                                                                                                                                                                                                                                                                      93.4%;
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hes 521;
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precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the major difference between these proteins and GAGE-1 (AAV05540) is the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAS for the first 112 bases. This region of GAGE-3 DNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or unine can be observed and then used to confirm a diagnosis of melanoma using cytolytic 7 cell clone proliferation methodologies.
                                     GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid encoding GAGE tumour rejection antigen precursor -processed by {\rm HLA}\text{-}{\rm CW6} molecules into peptides, useful to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCAGGGAGCTGTGTGGCGGTGCTGTG----TTCTTGCGTCCGGACTCTTTTCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence encodes a GAGE-2 tumour tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCCAGGGAGCTGTGAGGCAGTGCTGTGGTTCCTGCCGTCCGGACTCTTTTTTCCTC-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
cDNA encoding GAGE-2 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Den Eynde B, Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1e-12
0; Mismatches
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                                                                                                                                               location/Qualifiers
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/transl_except=
/transl_except=
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95.7%;
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Matches 518; Conserv
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The present sequence is one of a large number of S' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The S' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the S' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAs with intact S' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. S' ESTS are also used in diagnostic, forensic,
                                                                                                        419
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                                                                                                                                                                                                        474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                               ACCAATCACAGTGTTAAAAGAAGACATGTTGAAATGATGCAGGCTGCTCCTATGTTGGAA
                                                                                                                                                                                                                                                              235 CTCCAGCTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGCCTG
                                                                     295 AAGCTGAGAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTG
                                                                                                     360 ATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAGGTGAAA
                                                                                                                                      355 ATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGAAGAAAACGCCTGAAGAAGGTGAAA
                                                                                                                                                                       420 AGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAA
                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein 5' EST, SEQ ID NO: 2127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; chromosome mapping; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                         AAC02129 standard; cDNA; 430 BP.
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                                                                                                                                                                                                                                                                                                      A 540
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ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTA GACCAAGGCGCTATGTACAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCCGAGCAGTTCA GTGATGAAGTGGAACCAGCAACACCTGAAGAAGAGGGAACCAAGCAACTCAACGTCAGGATC

ACTGAGATTCATCTGTGTGAAATATGGCGAGGAAGATCGACCTATTATTGGCCTA

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TGCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCAAGGCGCTATGTACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iuman; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
  are used to obtain
                                                                                                                                                                                                                                                                                                                                ceccadadadererdaddedadadererdadarecridederecedadererrining
                                                                                                                                                                                                                                                                                                                                                                                    CTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCCAGGGAGCTGTGAGGCAGTGCTGTGGGTTCCTGCCGTCCGGACTCTTTTTCCTCTA
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                                                                                                                                                                                                                         Gaps
gene therapy and chromosome mapping procedures. They are used to obti
upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                         1;
                                                                                                                                                                DB 3; Length 430;
                                                                                                         Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                   Score 360.4; DB 3;
Pred. No. 4.9e-93;
5; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer agent-sensitive marker #105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodgkin's disease; glioma; ss.
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                                                                                                                                                                   66.78;
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                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be
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                                The invention relates to 1046 novel nucleic acids which are used as
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Claim 1; Page 120; 527pp; English
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 00%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:*
1: 9b ba:*

Minimum DB seq length: 0 Maximum DB seq length: 532 GenEmbl:*

1. gb ba:*
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3. gb_in:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6 350.8 65.9		BD0258	BD025874 Sequence
304.6 57.3			AX284300 Sequence
18 302.4 56.8		AX2846	AX284692 Sequence
174.2 32.7			AJ318881 Homo sapi
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1 150.6 28.3		BT007722	
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3 147.4 27.7		BD111325	
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Unclassified.
( Lases 1 to 532)
Van den Bynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and their
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C07K4/12, C12N15/09, C12P21/00, C12Q1/02, C12N15/00 CC
                                                                                                              organism='Homo sapiens (human)'.
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100.0%; Pred. No. 1.5e-127;
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   PC C07K4/12,C12N15/09,C12P21/00,C12Q1/C
Strandedness: Single,
CC Topology: Linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FH Key Location/Qualifiers
FT source 1. 532
PT /organism='Homo sapi
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Patent: US 5648226-A 17 15-JUL-1997;
Location/Qualifiers
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Sequence 17 from patent US 5648226.
IS5854
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12-JAN-1999 JP 2000528586
23-JAN-1998 US 09/012818
PIERRE VAN DER BENOIT VAN DEN EYNDE,OLIVIER DEBACKER,
THIERRY BOON FALLEUR
                                                                                                                                                                                                                                                                                                                 CATCTGTGTGAAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120
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I (bases 1 to 512)
Bruggen, P.V.D., Bynde, B.V.D., Debacker, O. and Falleur, T.B.
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof Patent: JP 2002509859-A 10 02-ARP-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
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         Patent: US 5858689-A 17 12-JAN-1999;
Location/Qualifiers
                                                                                   /mol_type="unassigned DNA"
                                                                /organism="unknown"
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JP 2002509859-A/10
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Van Den Eynde, B.J.
Van Den Eynde, B.J.

Direct Submission

Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute

for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium

for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
                                                                                                                                                                                                                                                                                                     GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180
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1 (Dases 1 to 524)
Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AGIGITIAAAAGAAGGCACGTIGAAATGATGCAGGCTGCTCCTATGTIGGAAATTIGTICA
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                                                                                                                                              1 AGCTGTGAGGCAGTGCTGTGGTTCCTGCCGTCCGGACTCTTTTTCC
                                                                       Score 532; DB 6; Length Fred. No. 1.5e-127; Mismatches 0; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="mRNA"
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100.0%; Pred. No. 1.5e-127;
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 /mol_type="unassigned DNA"
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2 (bases 1 to 528)
Van Den Eynde, B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
                                                                                                                                                                                                                                                                                                   61 CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new family of genes coding for an antigen recognized autologous cytolytic T lymphocytes on a human melanoma J. Exp. Med. 182 (3), 689-698 (1995) 95378788
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                                                                                                                                                   Score 517.4; DB 6
Pred. No. 9.2e-124
0; Mismatches 1
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                                                                         /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                          /organism="Homo sapiens"
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       Location/Qualifiers
1. .528
   Avalon Pharmaceuticals (US)
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Homo sapiens
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Best Local Similarity 99.8<sup>3</sup>
Matches 518; Conservative
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           /sex="female"
/cell_line="WZ2-MEL.43"
/tissue_type="melanoma"
/dev_stage="adult"
/5. .428
/codon_start="
/product="GAGE-5 protein"
/protein_id="AAA82748.1"
/db_xref="G1:914907"
/translation="MSWRGRSTYYWPRPRRYVQPPEVIGPMRPEQFSDEVEPATPEEG
EPATQRODPAAAOGGEBDEGASAGGGPKPEADSQEGGPPGTGCECDGPDGQEMDPNP
EEVKTPEEGEKQSQC"
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Cancer gene determination and therapeutic screening using signature
gene sets
Patent: WO 0194629-A 4660 13-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 09-JAN-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Horrigan, S., Soppet, D.R. and Weaver, Z.
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                                                                                                                                                                                                                                                                            98.5%; Score 524; DB 9; Length 524; 100.0%; Pred. No. 1.8e-125; ive 0; Mismatches 0; Indels
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xref="taxon:9606"
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2 birect Submission
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGWRGRSTYYWPRPRRYYOPPEVIGPMRPEQFSDEVEPATPEEG
BPATQRQDPAAAQEGEDBGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEVDPPNP
EEVKTPEEGEKQSQC"
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            coding for an antigen recognized
   A new family of genes coding for an antigen recognized autologous cytolyric T lymphocytes on a human melanoma U. Exp. Med. 182 (3), 689-698 (1995) 95378788
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99.6%; Pred. No. 2.4e-123;
iive 0; Mismatches 2;
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                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                           /cell_line="MZ2-MEL.43"
/tissue_type="melanoma"
/dev_stage="adult"
82. .435
                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                            /product="GAGE-6
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Epatgrodpaaagegedbgasagggpkpbadsgegghpgtgcecedgpdgemdppnp
BEVKTPEEGEKQSQC"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
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Pred. No. 9.2e-124;
); Mismatches 1;
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                                                                                                                                                                              /product="GAGE-4 protein"
/protein_id="AAA82747.1"
/db_xref="GI:914905"
                                  sapiens"
                                                                                 /sex="female"
/cell_line="MZ2-MEL.43"
                                                                                                              /tissue_type="melanoma"
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                                              /mol_type="mRNA"
/db_xref="taxon:9606"
Location/Qualifiers
                                                                                                                             /dev_stage="adult"
83. .436
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De Backer,O., Van den Eynde,B. and Boon-Falleur,T.
Isolated, truncated nucleic acid which are members of the
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Pred. No. 2.2e-120;
0; Mismatches 6;
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Location/Qualifiers
                                  CITITACAGCCTICTGCAAAGAAAAAAAAAA
                                                                 CTTTACAGCCTTCTGCAAAGAAAAAAA
                                                                                                                                                      528 bp
US 6509172.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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/organism="unknown"
                                                                                                                                                                   Sequence 1 from patent
AR275665
AR275665.1 GI:29709167
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Best Local Similarity 98.3%;
Matches 521; Conservative
                                                                                                                                                                                                                                                                            Unclassified.
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                                                                                                                                                                                     De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C., Czekay, S., Viars, C.S., De Plaen, B., Brasseur, F., Chomez, P., Van den Eynde, B., Boon, T. and van der Bruggen, P. Characterization of the GAGE genes that are expressed in various human cancers and in normal testis Cancer Res. 59 (13), 3157-3165 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSWRGRSTYYWPRPRRYVQPPEMIGPMRPEQFSDEVEPATPEEG
EPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGSEMDPPNP
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                  01-MAY-2000
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Catarrhini, Hominidae, Homo.
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Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
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                  linear
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          FLOWD Sapiens GAGE-7B mRNA, complete cds. AF055474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="GAGE-7B"
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/db_xref="G1:3511025"
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                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/codon start=1
                                                                    GI:3511024
                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 526)
De Backer, O.R.Y.
Direct Submission
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                                                                                                                         Homo sapiens
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/translation="MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDBVEPATPERGE
PATQRQDPAAAQEGEDBGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPE
EVKTPEEGEKQSQC"
                                                                                                       PRI 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                         GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG 360
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 530)

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                    527
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                                                                                                                                                                                                                                                                                            A new family of genes coding for an antigen recognized autologous cytolytic T lymphocytes on a human melanoma J. Exp. Med. 182 (3), 689-698 (1995)
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 496.8; DB 9;
Pred. No. 2.1e-118;
0; Mismatches 7;
                                                                                                                     Human GAGE-2 protein mRNA, complete cds
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/codon_start=1
/product="GAGE-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein_id="AAA82745.1"
/db_xref="GI:914901"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_line="MZ2-MEL.43"
/tissue_type="melanoma"
/dev_stage="adult"
84. .434
                                                                                                       530 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
1. 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="female"
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98.1%;
                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 514; Conserv
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                                                               RESULT 14
HSU19143
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                                                                          Mammalia; Butheria; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

1 Easter, O., Arden, K., Boretti, M., Vantomme, V., De Smet, C., Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van den Eynde, B., Boon, T. and van der Bruggen, P.

Characterization of the GAGE genes that are expressed in various human cancers and in normal testis

Cancer Res. 59 (13), 3157-3165 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSWRGESTYRERPERRYVEPPEMIGPMRPEQFSDEVEPATPEEGE"
PATORODPAAAQEGEDEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNPE
EVKTPEEGEKQSQC"
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B-1200, Belgium
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                                                                                                                                                                                                                                                           De Backer, O.R.Y.
Direct Submission

Direct (24-MAR-1998) Indwig Institute for Brussels Branch, 74 av. Hippocrate, Brussels Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 504.4; DB 9;
Pred. No. 2.2e-120;
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307 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG 366
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Copyright (c) 1993 - 2004 Compugen Ltd.
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bin/showiib.pl.cgi/response??libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 111

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This clone is available royalty-free from RZPD; contact RZPD (cloneGrzpd.de) for further information. Seq primer: M13x, Primer Sequence: TTTCACACACAGGAAACAGCTATGAC.
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Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human Vilgenesset - RZPD3

Unpublished (2003)

Contact: Ina Rolfs
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/clone lib="NHIB MGC 119"
/site_2 : BcokV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcokV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.93 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NH_MGC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 512.8; DB 12
Pred. No. 1.7e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                      sapiens"
                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
location/Qualifiers
                                                                                  organism="Homo
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Matches 525; Conserv
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/ Organizam="none saptens"
/ Ab xref="taxon:9606"
/ Alone="nones:30524555"
/ Lissue type="Pooled Chondrosarcoma Tumor cells"
/ Lib host="Pooled Chondrosarcoma Tumor cells"
/ Lib host="Delio Tip phage-resistant)"
/ Anote="Vector: pXx-Asc; Site 1: EcoRI; Site 2: NotI;
/ Note="Vector: pXx-Asc; Site 1: EcoRI; Site 2: NotI;
/ Library is oligo-dT primed and directionally cloned
Denatured RNA was size fractionated on a 1% agarose gel.
First strand CDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according tomRNA size fraction, ligated with
EcoR I adaptors, digested with Not I and then cloned
directionally into pXx-Asc vector. Average insert size
0.5-IKb. Adaptors 5 (AATTGGGCACAGG)3 and 5 d
CCTCGTGGTGCCS)3: 3: 3: Linker sequence - GCGGCGCTGAGAGCC T18.
                                                                                                                                                                                                            CF780547 S17 bp mRNA linear EST 20-OCT-2003
AGENCOURT 15739102 NIH MGC 217 Homo sapiens cDNA clone
IMAGE:30524555 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Betheada, WD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information action through the I.M.A.G.E. Consortium/LiNL at:
http://image.llni.gov
Plate: NDAMG04 row: e column: 12
High quality sequence stop: 517.
GAAGGCACGTTGAAATGATGCAGGCTGCTATGTTGTTGGAAATTTGTTCATTAAAATTCT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing primers 3'end: 13 promoter primer 5'd (ATTAACCCTCACTAAAGGA)3'. 5' End: T7 promoter primer 5'd (TAATAACGACTCACTAAAGGA)3'. Average insert size 0.5-1kb. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                          481 CCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAAAAA 520
                                                                 CCCAATAAAGCTTTACAGCCTTCTGCAAAAAAAAAA 530
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Best Local Similarity 99.2
Matches 509; Conservative
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603322594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 TTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAA 484
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NIH-MGC http://mgc.nci.nih.gov/.
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/tissue type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH1 MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally, oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llh.gov.rem.l column: 24
TGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCCGAGCAGTTCAGTGATGAAGTGGA
                                                                                                                                                    124 IGTACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCCGAGCAGTTCAGTGATGAGTGGA
                                                                                                                                                                                                                        ACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCTGCTGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="Soares testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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hd39d05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 CCGGACTCTTTTCCTCTACTGAGATTCATCTGTGTGAAAATATGAGTTGGCGAGGAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                 89.5%; Score 476.4; DB 9; Length 489; 99.6%; Pred. No. 2.4e-96; ive 0; Mismatches 1; Indels 1;
                                       'organism="Homo sapiens"
                                                                          'db xref="taxon:9606"
                                                                                             'clone="IMAGE:782636"
 Location/Qualifiers
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                                                                                                                   sex="male"
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Matches 488;
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AW510753/c
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Mocre,B., Schellenberg,K., Lennon,G., Marra,M., Martin,J., Morie,Y., Wylie,T., Waterston,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Theising,B., Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LiNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 Hd. ET from Amersham
High quality sequence stop: 427.
                                                                                                                                                                                                           195 TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAGGAGGAGAGAAGAACATCTGCAGGTCAAGGGCTGAAGCCTGAAGCTCATA
                                                                                                             AGCTGTGAGGCAGTGCTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
                                                                                                                                       AGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGCTCCGGACTCTTTTTCCTCTACTGAGATT
                                                                                                                                                                                        CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC
                                                                                                                                                                                                                                                              121 GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAG
                                                                                                                                                                                                                                                                                                                                        TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                               CTCAGGAGGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATA
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                                                                            Gaps
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                                       DB 12; Length 509;
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                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Email: est@watson.wustl.edu
                                   Score 490.2; DB 12;
Pred. No. 1.9e-99;
0; Mismatches 3;
                                                                        0;
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                                   92.1%;
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                                   Query Match
Best Local
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AA447559/c
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                         LOCUS
DEFINITION
         AA738037/c
                                                                                                                                                ORGANISM
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TITLE
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                                                                                                                                                                                                                                                                                                                                /lab_host="DH109"
/clone lib="Soares NFL T GBC S1"
/clone lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker, Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCL CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CNNAs from pools of 5,000 clones made
from the same 3 libraries The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGT 127
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
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                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 ACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGCAGGAGGATGGA
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                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2911881"
                                                                                                                                                                                                                             Location/Qualifiers
1..457
                                                                                                      Tumor Gene Index
Unpublished (1997)
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Matches 45
                                                                                                                                                                                                                                                Source
ORGANISM
                                                 REFERENCE
                                                                   AUTHORS
                                                                                                                     JOURNAL
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                                                                                  TITLE
                                                                                                                                     COMMENT
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RESULT

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-ramail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llml.gov/bbrp/image/image.html

Insert Length: Sll Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 435.
464 bp mRNA linear EST 22-JAN-1998 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1256204 3' TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Glome_libe="NGI_CGAP_GG3"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                     1 (bases 1 to 464)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 CCTGAAGTGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGGACCAAGGCGCTATGTACAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 ATGAGTTGGCGAGGAAGATCGACCTGTTATTGGCCTAGTCCAAGACGCTATGTACAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1256204"
/tissue_type="pooled germ cell tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 443.6; DB 9;
Pred. No. 5.3e~89;
0; Mismatches 9;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="DH10B"
                                                                                                AA738037.1 GI:2768794
EST.
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98.0%;
                                                                                                                                                            Homo sapiens (human)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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similar to 7
AA738037
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88 GAAGATCGACCTATTATTGGCCTAGGCCGCTATGTACAGCCTCCTGAAGTGATTG 147
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                                                                                                                                                                                                      CAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCAC 438
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                                                            267 AGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACC
                                                                                                                                                                                                                                                                                                GITGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAA 498
                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4451958"
/tissue type="adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone lib="NH1 MGC 90"
/note="Corgan: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG120336 480 bp mRNA linear EST 30-JAN-20
602353732F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451958 5',
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                                                                                                          CACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAAATC
                                                                                                                                                                                                                                                    147 cagaddagardaaaacgccrgaagaagargrgaaagcaarcacagrgrraaaagaagacac
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                   AGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dental: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lettp://image.llhl.gov
thtp://image.llhl.gov
High quality sequence stop: 480.
High quality sequence stop: 480.
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99.1%; Pred. No. 7e-88;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 AGCTTTACAGCCTTCTGCAAAGAAAA 525
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db xref="taxon:9606"
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ORGANISM
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AUTHORS
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KEYWORDS
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//Lab host="DH108"
//Lob lib="Soares NFL T GBC S1"
//Lob lib="Organ: pooled; Vector: p7773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco R1; Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbH119W, testis NHT, and B-cell
libraries (fetal lung NbH119W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from pools of 5,000 clones made
from the same 3 libraries The pools consisted of
I.M. AGE. Clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 AAATGATTGGGCCTATGCGGCCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 447)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                AI381509 447 bp mRNA linear EST 28-MAR-:
te76b07.x1 Soares NFL T GBC_S1 Homo sapiens cDNA clone
IMAGE:2092597 3' Similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACATG
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                                                                           GCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCA
                                                                                                                    104 GCACGTICAAAIGAIGCAGGCIGCICCIAIGIIGGAAAITIGIICATIAAAAITCICCCA
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                                                                                                                                                                    495 ATAAAGCTTTACAGCCTTCTGCAAAGAAAAAAAA 532
                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2092597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
A1381509
A1381509.1 GI:4194290
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Unpublished (1997)
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Matches 44
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Length 505;
                      Score 436; DB 14;
Pred. No. 2.7e-87;
0; Mismatches 10;
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 331.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 AAATGTTGCAGGCTGCTCCTATGTTGAAACT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 AAATGATGCAGGCTGCTCCTATGTTGGAAATT 474
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/db_xref="taxon:9606"
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                     82.0%;
97.8%;
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                     Query Match
Best Local Similarity 97.8
Matches 442; Conservative
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Unpublished (1997)
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AA760996/c
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K-EST0159805 L8SCK0 Homo sapiens cDNA clone L8SCK0-8-B09 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell line="SCK"
/lab_host="Top10F'"
/clone lib="LaSCKO"
/note="Organ: Liver: Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI, The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-8066. RNA was prepared from harvested cell
culture."
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                             180
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                          GCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACAACACCTGAAGAAGAGGG 120
                                                                      AACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCAT 267
                                                                                                                                             CTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGGTCACCCAACAGACTG 327
                                                                                                                                                                            CTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCACAGACTG 240
                                                                                                                                                                                                                                                      241 GGTGTGAGTGTGAAGATGGTCCTGATGGCCAGGAGATGGACCCGCCAAATCCAGAGGAGG 300
                                                                                                                                                                                                                                                                                                                 507
                                                                                                                                                                                                                                                                                                                                                                                        361 AIGCAGGCIGCTCCTAIGTIGGAAATTIGTTCATTAAAATTCTCCCCAATAAAGCTTTACA 420
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
GGCCTATGCGGCCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACTGAAGAGGGG
                                                                                                         388 TGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATG
                                                                                                                                                                                                                                                                                                                                                                   448 ATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACA
                                                                                                                                                                                                                    GGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGGATGGACCCGCCAAATCCAGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21C Frontier Korean EST Project 2001
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 8 row: B column: 09
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L8SCK0-8-B09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +82-42-860-4470
Fax: +82-42-860-4409
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Contact: Kim YS
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KEYWORDS
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ORIGIN

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AA760996 450 bp mRNA linear EST 26-JAN-1998 nx32h08.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
   o;
                                                                                                                                                                                            GCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGT 142
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NCI-GARP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                           19 Genechecenceacherrinierenenacheannenenenenenananananen
                                                             GTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATTCATCTGTGTGAAATATGAGTTG
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Indels
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ORIGIN

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AW016546 418 bp mRNA linear EST 10-SEP-1999 UI-H-BIOp-abg-g-06-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone INAGEs:2711986 3', mRNA sequence.
AW016546.1 GI:5865303
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
Insert Length: 504 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 391.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  /clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
pyllinker, Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/TI3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCCACAGACTGGGGTGTGAGATGATGGTCCTGATGGGCAGGAGATGGACCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 ANTCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCCCAGTGTTAAAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 GCACGTTGAAATGATGCAGGCTGCTCTATGTTGGAAATTTGTTCATTAAAATTCTCCCA
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Pred. No. 4.8e-83;
0; Mismatches 10;
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                                                                                                                                                                                              1. .455
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                     clone="IMAGE:1751408"
                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%;
llarity 97.4%;
Conservative
                                                                                                                                                                                                                                                                                                              /sex="male
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445; Conserv
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                          /lab host="DH10B" / Clone lib="NCI CGAP GC4" / Anote="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI187350 455 bp mRNA linear EST 10-NOV-1998 qf29a05.xl Soares testis NHT Homo sapiens cDNA clone IMAGE:1751408 3' similar to SW:GGE4 HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                              1,
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Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                           Score 431.6; DB 9; Length 450;
Pred. No. 2.6e-86;
0; Mismatches 5; Indels 1
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Email: cgapbs-r@mail.nih.gov
DNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
            tumors"
         type="pooled germ cell
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Conservative 0
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Matches 445;
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Email: cgapbs-r@mail.nih.gov

The sequence contained an oligoor

Oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:

I.M.A.G.E. Consortium/Lin. at:

www-bio.llnl.gov/bbrp/image/image.html
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                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI_CGAP_Col0 pool 1 LLAM 2644-2653, 2871-2872 (IMA ClonelDs 1057416-1061255, 1144584-1145351) The resuls subtracted library contained 4 million recombinants Subtraction was performed as previously described
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Genome Research 6, 791-806.
                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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TAG_TISSUE=germ cell
TAG_LIB=NCI CGAP_GC4
TAG_SEQ=AAATC"
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                 sapiens (human)
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                                                                                                             Tumor Gene Index
Unpublished (1997)
                              Homo sapiens
                                                                                                                                                                                                                                                                                                         source
                            ORGANISM
                                                                    REFERENCE
                                                                                   AUTHORS
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AA868226 426 bp mRNA linear BST 16-MAR-1998 ak48h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409245 3' similar to SW:GGB2_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIANL at:
www-bio.llnl.gov/bbrp/image/image.html
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/lab host="DH10B"
/clone lib="Soares testis_NHT"
/clone="Vector: pT7T30-Pac" (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                       298 AGCTGCTCAGGAGGAGAGGAGGAGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGC 239
                                                                                                                                                                                                                                                                                                                                                                                     358 TGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 GCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 ATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTT 475
418 AAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGA 359
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 ATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTT
                                                              TGAAGTGGAACCACCACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGC
                                                                                                                                                                                              236 AGCTGCTCAGGAGGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGC
                                                                                                                                                                                                                                                                                                                                 296 TGATAGCCAGGAACAGGGTCACCCACAGACTGGGGTGTGAGTGTGAAGATGGTCCTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1409245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .426
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175

0;

Length 418; Indels

DB 9;

76.6%; Score 407.4; DB 9; 98.6%; Pred. No. 6.8e-81; iive 0; Mismatches 6;

Conservative

Query Match Best Local Similarity Matches 411; rgriaccaarcigaagigggagcggccgcccaarittrittittitti 3'].

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eloned into the Not I and Elone into the Modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 383)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 GATIGGTCCTGATIGGGCAGGAGATIGGACCCGCCAAATICCAGAGGAGGTGAAAACGCCTGAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 bp mRNA linear EST 06-MAR-200
ESTOIL1762 SSSNU484s1 Homo sapiens CDNA clone SSSNU484s1-15-D07
BM836228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGGIGAAAAGCAAICACAGIGIIAAAAGAAGGCACGIIGAAAIGAIGCAGGCIGCICC 61
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAACTTTACAGCCTTCTTCAAAAA 1
                                                                                                                                                                                                                                                                                                          TATCGGCCTAGACCCAAGACGCTACGTAGGCCTCCTGAAATGNANTTGCCTATGCGGCCC
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                               Length 426;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                         Score 398.8; DB 9;
Pred. No. 5.7e-79;
0; Mismatches 14;
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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/db_xref="taxon:9606"
/clone="S5SNU484s1-15-D07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .383
/organism="Homo sapiens"
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Plate: 15 row: D column: 07
High quality sequence stop: 383.
Location/Qualifiers
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96.7%;
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                               Query Match
Best Local Similarity
Matches 406; Conserv
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JOURNAL
COMMENT
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BM836228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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/clone libe SSSNU48481"
//clone Stomach; Vector: pTZ18RP1; Site 1: ECORI;
Site 2: Not1; The poly (A) + RNA was decapped with that babacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The dT-RNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Toplof' by electroporation method.
After analyzing and sequencing about 2,000 ~ 3,000
colonies in original cDNA library, the abundant cDNAs were
selected and amplified by PCR reaction using vector region
primer including T7 promotor as 5, primer and NUT) 14 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Justice including 1' promotor as primer and middle of synthesis of biotinylated single stranded RNA by in vitro synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. subtracted cDNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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Pred. No. 2.9e-74;
0; Mismatches 2; Indels
                 /cell_type="Epithelial"
/cell_line="SNU-484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, 2004, 20:52:27
                                                                         host="Top10F'"
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tissue
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Job time: 2417 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August on: Run

6, 2004, 18:20:25 ; Search time 333 Seconds (without alignments) 6786.911 Million cell updates/sec

US-09-782-745-17 Perfect score: Title:

1 AGCTGTGAGGCAGTGCTGTG........CTGCAAAGAAAAAAAAA 532 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

3373863 seqs, 2124099041 Searched:

4998588 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 532

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq 29Jan04:* geneseqn1980s:* Database

geneseqn2001as:*
geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* geneseqn1990s:*
geneseqn2000s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			Lund	Human		N	Ada15801 Human GAG		ď	Human	Human	Group	Group	ம	TPS1 S	TPS1			Human	3 Group	5 Differ		Human
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Aai60530 Human pol	Abz19538 Group III	Aas69484 DNA encod	Abt15728 Human can			Abk38062 cDNA enco	Aca10391 Human lun		Ade72125 Human lun	Aad24228 Human dif	Aba92217 Melanoma				_	Aca59708 Prostate	Ab195271 Human P10	Acc95435 Prostate	Adb13922 Human pro	Human	Human
AA160530	ABZ19538	AAS69484	ABT15728	AAD14981	AAF68151	ABK38062	ACA10391	ABX99342	ADE72125	AAD24228	ABA92217	AAH93807	AAS63900	AAH02872	AAH85121	ACA59708	ABL95271	ACC95435	ADB13922	AAS24637	AAH83260
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183.6	171	164.2	140	133.2	108	108	108	108	108	103.6	103.4	101.6	101.6	101.6	101.6	101.6	101.6	101.6	101.6	100.8	100.8
24	25		27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAX90522 standard; cDNA; 532 BP. (first entry) 30-SEP-1999 AAX90522; RESULT 1 AAX90522

GAGE-5 tumour rejection antigen clone nucleotide sequence.

Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte; GAGE; ss.

Homo sapiens.

WO9937665-A1.

29-JUL-1999.

99WO-US000775. 12-JAN-1999;

98US-00012818.

23-JAN-1998;

(LUDW-) LUDWIG INST CANCER RES.

Boon-Falleur T; Debacker O, Van Den Eynde B, Van Der Bruggen P,

WPI; 1999-469111/39.

tumor New isolated peptides which bind to HLA-A29 molecules, which are trejection antigens used for detection and therapy of pathological conditions, e.g. cancer.

Example 13; Fig 4; 62pp; English.

The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present

Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 U; 0 Other;

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Debacker O,
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                                                                                                                   GCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCCGAGCAGTTCAGTGAAG
                                                                                                                                 GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
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/*tag= a
/transl except= (pos:189. .191, aa:Ala)
/transl_except= (pos:192. .194, aa:Thr)
        Score 532; DB 2; L
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The present sequence encodes a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In precursor and the only normal tissue which expresses GAGE TRAP protein is contrast the only normal tissue which expresses GAGE-1 TRAP protein is and captured (see AAV1817-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5 end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic 7 cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants
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   Van Den Eynde B,
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99.1%;
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Best Local Similarity
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agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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Best Local Similarity
Matches 518; Conserv
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                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horrigan S;
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                                                          related gene sequence SEQ ID NO:4660.
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             ABL66323 standard; DNA; 528 BP.
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Soppet DR,
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The present invention describes a method (MI) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is anti-neoplastic agent, and can be used for producing a product which is anti-neoplastic agent. MI can be used in the treatment of cancer such to properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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Pred. No. 9.3e-140;
0; Mismatches 1;
Claim 1; SEQ ID NO 4660; 44pp; English
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                                                                                                                                                                                                                                                                                                                            Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynucleotide or antibody.
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                                   Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
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             bladder cancer associated cDNA sequence SEQ ID NO:144.
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Pred. No. 2.7e-139;
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                                                                                                                                                              03-JUL-2001; 2001US-0302814P.
03-AVG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
12-AVG-2001; 2001US-0350666P.
                                                                                                                                                                                                                                         (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                      03-JUL-2002; 2002WO-US021338
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08-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polymucleotides and polypeptides are used for identifying a compound that medulares a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful
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GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGATGAAGATGGTCCTGATGGGCAGG
                                                             GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCCAGG
                                                                                                                                                                                                         AGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGGAGGTGAAAAGCAATCAC
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                                                                                                                                                                                                                                                                                                                                               AGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTTGTTCA
                                                                                                                                     AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGG
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-033245P.
13-NOV-2001; 2001US-0334370P.
29-NOV-2001; 2001US-0334370P.
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           lung cancer or other benign or precancerous lesions, e.g. atelectasis, emplyyeams, bronchits, chronic obstructive pulmonary disease, librosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynuclectides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynuclectides of the
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treating lung cancer, such as small cell lung cancer, non-small cell
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human leukocyte antigen, HLA; tumour rejection antigen precursor;
major histocompatibility complex; MHC; cytolytic T cell proliferation;
chromosome Xp11.2-p11.4.
                                                                                                                                                                                                                                                                                                                                                                                 CTCAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTGATA
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                                                                                                                                                                                                                                                                                     GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
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                                                                                                                    Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0 U; 0 Other;
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                                                                                                                                         Score 515.8; DB 7;
Pred. No. 2.7e-139;
); Mismatches 2;
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The invention relates to isolated GACE-7B and GAGE-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic Tlymphocytes (CTLS) or determining if CTLS are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte artigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents CDNA encoding the human GAGE-7B polypeptide of the invention. The gene resides on chromosome Xp11.2-p11.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tume rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
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/product= "Human GAGE-7B"
/transl except= (pos:115. .162, aa: GPMRPEQGSDEVPEMI)
/transl_except= (pos:265. .306, aa: HPQTGKPEAHSQEQ)
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Pred. No. 2.9e-137;
0; Mismatches 2;
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Local Similarity 99.6%;
les 510; Conservative (
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                           TGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTTCTCCCAATAAAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid that encodes a human leukocyte antigen (HLA) molecule. The GAGE-7B and GAGE-8 nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents obna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
                                                                                                                                                                                                                                                            Human; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;
human leukocyte antigen; HLA; tumour rejection antigen precursor;
major histocompatibility complex; MHC; cytolytic T cell proliferation;
chromosome Xpl1.2-pl1.4.
           TGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAG
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aa:Lys)
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/transl_except= (pos:244.
/transl_except= (pos:400.
                                                                                CTTTACAGCCTTCTGCAAAGAAAAAAAAAA
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P-PSDB; ADA15778.
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Length 528;

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94.8%; Score 504.4;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
immune response; virology; immunology; microbiology; molecular biology;
recombinant DNA technology; gene; ss.
                                                                                                                                                                                                                                                                                              CAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGCCGAAGCCTGAAGCTGATAGC
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); Mismatches 6;
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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P-PSDB; ABP54447.
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AB017575 to AB020506 represent isolated polynucleotide (I) sequences, and ABP54446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology,
                                                                                                                                                                                                                                                  immunology, microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
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New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and virology, immunology, microbiology, molecular biology and recombinant
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                                                                                                                                                                                                                                                                                                                                                                                     Score 496.8; DB 7; Length 530;
Pred. No. 8.9e-134;
0; Mismatches 7; Indels 3,
                                                                                                                                                                                                                                                                                                                                                   Sequence 530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
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                                                                                        Claim 1; SEQ ID NO 2890; 207pp; English.
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Best Local Similarity 98.1%;
Matches 514; Conservative
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mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact by ESTs are also used in diagnostic, formeric, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAAYGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATNA-YGGCCTAGACCAAGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCCGAGCAGTTCAGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 GCTATGTACAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGGAGCAGTTCAGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGGAGGGAGAGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAAGATGTGAAGATGGTCCTGATGGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted novereine and many terms of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accretasascasascretarestricersecestecesacretriritecretarerererer
                                                                                                                                                                                                                                                                                                                                                                                             diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                           nucleic acid that is a 5' expressed sequence tag (5' EST) for tining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 134 G; 85 T; 0 U; 8 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.9e-91;
5; Mismatches 3;
                                                                                                                                                                                                                                                                Giordano J;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.9%;
97.6%;
                                                                                                                                                  21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                       99US-0122487P
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                                                                                                                                                                                                                                                                Dumas Milne Edwards J,
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                                                                                                                                                                                                                                                                                                                      P-PSDB; AAG02123
                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                       26-FEB-1999;
                                     Homo sapiens,
                                                                         EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                           obtaining
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AGATGGAMC 430

422

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

CTGAAGNTGATAGCCAGGAACAGGGTCNCCCCCANACTGGGNGTNAGTGTNAAAATGGTC 270

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269 409

CTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTG CTNATGGGCAGNANATGGACCCNCCAAATCCAAAGNAGGTGAAAACNCCTGAANAAGGTG AAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTG 468

209 AAAAGCAATCCCAGTGTTAAAANAAGGCNCGTTGAAATGATGCAGGCTGCTCCTATGTTG GAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAAAAAA

528

GABATITGIICAITAAAAITCTCCCAATAAAGCIITACAGCCIINNAAAAAAAAAAAA 90

529 AAAA 532

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RESULT 11 AAS60496/

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particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemcherapeutic compounds. The markers can also be used as targets in developing treatments for cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers
                                                                                                                                                                                               cell marker; TAXOL; cytostatic; tumour; carcinoma; carcinoma; sarcoma; fibrosarcoma; leukaemia; eukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid, used as a marker to determine the effectiveness of using TAXOL to treat cancer cell growth in individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 1046 novel nucleic acids which are used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Huffel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                            Human cancer agent-sensitive marker #105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 120; 527pp; English.
                                         AAS60104 standard; cDNA; 530 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolt A,
                                                                                                                                                                                                                                                       Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-2001; 2001WO-US012132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-2000; 2000US-0197538P.
                                                                                                                   (first entry)
                                                                                                                                                                                                                                       leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-602933/68.
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Best Local Similarity
Matches 322; Conserv
                                                                                                                                                                                                                                                                                                                                        WO200179556-A2.
                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                      cell
                                                                                                                     29-JAN-2002
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                                                                                                                                                                                                                                       vmphocyti
                                                                              AAS60104;
                                                                                                                                                                                                 Human;
RESULT 10
AAS60104/c
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Human cancer agent-sensitive marker #227.

(first entry)

29-JAN-2002

AAS60496;

AAS60496 standard; cDNA; 365 BP.

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markers can also be used as targets in developing treatments for cencer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid, used as a marker to determine the effectiveness of TAXOL to treat cancer cell growth in individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to 1046 novel nucleic acids which are used as
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 231; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    using
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Gaps

5;

Indels

Score 304.6; DB 4; Length 530;

.6; L-5.4e-78; 40;

Pred. No. 5.4e 0; Mismatches

57.3%;

Conservative

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markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The
Human, cancer cell marker; TAXOL, cytostatic; tumour; carcinoma; squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia; lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Huffel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                    Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bolt A,
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                                                                                                                                                                                                                                                                                                                  WO200179556-A2.
                                                                                                                                                                                                                                Homo sapiens
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(CORI-)
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                                                                                                                                  GCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGGAAAGGATAAGGGAGCATCTGCA 306
                                                                                                                                                         GGTCAAGGGCCCGAAGCCTGATAGCCAGGAACAGGGTCACCCCACAGACTGGGTGT 332
                                                                                                                                                                                    246
                                                                                                                                                                                                                              GAGTGTGAAAATGGTCCTGATGGCAGGAAATGGACCCGCCAAATCCAAAGGAGGTGAAA 186
                                                                                                                                                                                                                                                          452
                                                                                                                                                                                                                                                                             ACGCCTGAAGAAGCTGAAAAGCAATCTCAGTGTTAAAAAAAGGCACGTTGAAATGATGCA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA
                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cancer, tumour, therapy, diagnosis, CT antigen, CP antigen;
immune response, virology; immunology; microbiology; molecular biology;
recombinant DNA technology; gene; ss.
                                                                                                           213 GCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCA
                                                                                                                                                                               305 GGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCCCAGACTGGTGT
                                                                                                                                                                                                                                                                                                      GGCTGCTCCTATGTTGGAAATTTGTTCATAAAATTCTCCCAATAAAGCTTTACAGCCTT
      the
                                                                                                                                                                                                                                                      393 ACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGCACGTTGAAATGATGCA
                                                                                                                                                                                                                                                                                                                            GGCTGCTCCTATGTTGTTCATTAAATTCTCCCAATAAAGCTTTACAGCCTT
                                                                                       Gaps
      one of
                                                                                       °,
                                                               Length 365;
disease and tumours (e.g. glioma). The present sequence is 1046 novel cancer cell markers
                                                                                      11; Indels
                                     BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group III cDNA cancer related clone SEQ ID NO:1977.
                                                             Score 302.4; DB 4;
                                                                        Pred. No. 2e-77;
                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1977; 207pp; English
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                                                                                                                                                                                                                                                                                                                                                     CTGCAAAGAAAAAAAA 532
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                                                             56.8%;
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ19551 standard; cDNA; 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                       Local Similarity 96.6
les 309; Conservative
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                                                             Query Match
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ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and ABP5446 to ABP54472 represent protein (II) sequences, from the present thorention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for immunology, microbiology, molecular biology and recombinant DNA, immunology, microbiology, molecular biology and recombinant DNA, techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response; virology; immunology; microbiology; molecular biology; recombinant DNA technology; gene; ss.
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                                                                                                                                                                                                                                                                                                     Score 237; DB 7;
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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Best Local Similarity 100.
Matches 237; Conservative
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Claim 1; SEQ ID NO 2181; 207pp; English.
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                ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and ABP5446 to ABP54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAG 180
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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ABD17575 to ABD20506 represent isolated polynucleotide (I) sequences, and ABD54446 to ABD54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for similaring immune response. They an also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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Pred. No. 4.7e-58;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 264 BP; 64 A; 66 C; 75 G; 59 T; 0 U; 0 Other;
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
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Best Local Similarity
Matches 236; Conservat
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Claim 1; SEQ ID NO 2950; 207pp; English

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ABD17575 to ABD20506 represent isolated polynucleotide (I) sequences, and ABD54446 to ABD54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I), (II), antibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, incrobiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.Wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 IGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTA 128
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                                                                                                                                                                                                                                                                                                                                         Score 227.4; DB 7; Length 229; Pred. No. 9.2e-56; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                   Sequence 229 BP; 56 A; 55 C; 64 G; 54 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           42.7%;
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.6
Matches 228; Conservative
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Search completed: August 6, 2004, 19:34:18 Job time : 335 secs

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Sequence 16, Appl
Sequence 2127, Ap
Sequence 20, Appl
Sequence 695, Appl
Sequence 485, Appl
Sequence 475, Appl
Sequence 475, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 477, Appl
Sequence 477, Appl
Sequence 477, Appl
Sequence 487, Appl
Sequence 481, Appl
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-473-603-38

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US-10-821-234-695

US-10-821-234-695

US-10-453-372-485

US-10-453-372-475

US-09-970-607-44

US-09-970-607-44

US-09-970-607-44

US-09-570-7378-472

US-09-570-7378-472

US-10-453-372-477

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US-10-453-372-487

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Seguence 46. Appl				421	613,	31.		32.	140,	5858								207	27194	
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78.6	57	53	51	49.4	49.4	48.8	48.2	45.6	43.6	41.6	40.2	39.6	39	38.6	36.6	36		36	35.4	35.2
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ALIGNMENTS

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                                                                           APPLICANT: Wang, Yixin
TITLE OF INVENTION: Colorectal Cancer Prognostics
TITLE REPERENCE: VDX-5002 CIP
CURRENT APPLICATION NUMBER: US/10/782,413
CURRENT FILING DATE: 2004-02-18
PRIOR APPLICATION NUMBER: 10/651,237
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 94
SEQ ID NO 16
LENGTH: 528
                                                                                                                                                                                                                                                                                                                                             97.3%; Score 517.4; DB 7;
99.8%; Pred. No. 1.7e-149;
live 0; Mismatches 1;
                              ; Sequence 16, Application US/10782413; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 518; Conserv
                                                                                                                                                                                                                                                                                         ; ORGANISM: human
US-10-782-413-16
RESULT 1
US-10-782-413-16
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                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                   Score 350.8; DB 7;
Pred. No. 4.9e-98;
5; Mismatches 3;
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Sequence 38, Application US/10473603
GENERAL INFORMATION:
APPLICANT: OLD, Lloyd
APPLICANT: SCANLAN, Matthew
APPLICANT: SCANLAN, TACTESTIS ANTIGENS; FILE REPRENCE: L0461.701550300
CURRENT APPLICATION NUMBER: US/10/473,603
CURRENT FILING DATE: 2003-09-30
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2002-01-22
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-04-30
PRIOR PRILING DATE: 2001-04-30
PRIOR PILING DATE: 2001-04-30
                                                             LOCATION: 36
OTHER INFORMATION: Xaa=Glu or Lys
                                                                                                                                                                    CTHER INFORMATION: Xaa=Asp or Glu US-10-793-479-2127
OTHER INFORMATION: Xaa=Cys or Arg
                                                                                                                                                                                                                                      Query Match 65.9%;
Best Local Similarity 97.6%;
Matches 360; Conservative
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AGATGGAMC 430
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                    FEATURE:
NAME/KEY: UNSURE
                                                                                                                             NAME/KEY: UNSURE LOCATION: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-473-603-38
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                                                                                                               AGTGTTAAAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
                                                                                                                                                                                                   481 TTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAA 519
                                                                                                                                                                                                                               489 TIAAAATICICCCAATAAAGCTITACAGCCTICTGCAAA 527
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OTHER INFORMATION: k=g or
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OTHER INFORMATION: r=a or
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OTHER INFORMATION: n=a,
FEATURE:
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NAME/KEY: misc_feature
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NAME/KEY: CDS
LOCATION: 202..429
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                                                                                                                                                                                                                                                                                                                   RESULT 2
US-10-793-479-2127
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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT PILING DATE: 2004-04-07
FRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOP IN NOS: 1704
SEQ ID NOS: 1704
SEQ ID NOS: 136
                                                                                                                                TGAGTTGGCGAGGAAGATCGACCTATATTGGCCTAGACCAAGGCGCTATGTACAGCCTC 135
                                                                                                                                                                           readrigadeardrahachagarecenaricereanhagagahargaeah---handrer 144
                                                                                                                                                                                                                         CTGAAGTGATTGGGCCTATGCGGCCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACAC 195
                                                                                                                                                                                                                                                                                                                  196 CTGAAGAAGGGGAACCCAGCAACTCAAGGATCCTGCAGGTGCTCAGGAGGGAAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 ACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAA 375
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                                                                                  chrodrichricaacarchrometrichchchchchchchchchchchchchchchch
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                                         CTGTGTGGTTCCTGCCGTCCGGACTCTTTTCCTTCTACTGAGATTCATCTGTGTGAAATA
                                                                                                                                                                                                                                                                                                                                                              193 GİCAAGAAGAAÇCACCAACIGATAATCAGGGTATTGCACCIAGTGGGGAGATCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 695, Application US/10821234 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 25
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                                                                                                                                                                                     AGTIGGCGAGGAAGAICGACCIATTATTGGCCTAGACCAAGGCGCTATGIACAGCCTCT 137
                                                                                                                                                                                                                              80 ATTIGGCGAGGAAGATCAAC---ATATAGGCCTAGGCCGAGGAGAAGATGTACCACCTCCT 136
                                                                                                                                                                                                                                                                              GAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACT 197
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                                                                                           GIGIGGITCCIGCCGICCGGACTCTTTTTCCTCTACTGAGATTCATCTGTGAAATATG
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            Length 520;
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Pred. No. 8e-33;
0; Mismatches 190; Indels
                                                       Indels
                                                                                                                                                                                                                                                                                                                          137 GAGCTGATTGGGCCTATGC-----TGGAGCCCGGTGATGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAAAAGCITIACAGCCITCIGCAAAAAAAAAAAA 532
  Score 208.4; DB 8;
Pred. No. 5.7e-54;
0; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OLD, Lloyd
APPLICANT: SCANLAN, Matthew
APPLICANT: SCANLAN, Matthew
APPLICANT: CLEN, Yao-Tseng
APPLICANT: CLEN, Yao-Tseng
TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
FILE REFERENCE: L0461.70155US00
CURRENT APPLICATION NUMBER: D6/10/473,603
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: PCT/US02/09808
PRIOR APPLICATION NUMBER: 60/280, 718
PRIOR PILING DATE: 2002-01-22
PRIOR PELING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR PRILICATION NUMBER: 60/285,154
PRIOR FILING DATE: 2001-03-30
PRIOR PRILICATION NUMBER: 60/285,154
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/285,154
PRIOR FILING DATE: 2001-03-30
PRIOR PRILICATION NUMBER: 60/285,154
PRIOR FILING DATE: 2001-03-30
PRIOR PRILICATION NUMBER: 60/285,154
PRIOR FILING DATE: 2001-10-05
NUMBER: OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/10473603 GENERAL INFORMATION:
39.2%;
69.9%;
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                                                  Conservative
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Best Local Similarity 59.1'
Matches 305, Conservative
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                                                362;
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LENGTH: 528
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GENERAL INFORMATION:

APPLICATION:
APPLICATION:
APPLICATION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOI CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2001-02-30
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/18567
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-05-31
PRIOR PILING DATE: 2001-06-24
PRIOR PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR PILING DATE: 2001-08-24
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                                                                                                                                                       AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC 420
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                                                                                                                                                                                                                                                                                                421 AGTGTTAAAAGAAGGCACGT----TGAAATGATGCAGGCTGCTCCTATGTTGGAAATT 474
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                                                                               239 pacaddaaciddecicigcilaadaladadacaddaciddaddigdiccidaidicagdd 298
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                     301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSequist version 0.1
SEQ ID NO 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 475;
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Pred. No. 9.6e-31;
0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 485, Application US/10453372; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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GENERAL INCOMMATION:

APPLICANT: Malyankar et al.

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-675 CIP2

CURRENT APPLICATION NUMBER: US/99/970,607

CURRENT FILING DATE: 2001-10-03

PRIOR APPLICATION NUMBER: 60/182,734

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-02-23

PRIOR PLING DATE: 2000-02-33

PRIOR PLING DATE: 2000-02-33

PRIOR APPLICATION NUMBER: 60/184,497

PRIOR FILING DATE: 2000-02-34

PRIOR FILING DATE: 2000-02-34

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-34

PRIOR PLING DATE: 2000-02-34

PRIOR PLING DATE: 2000-04-13

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CCTCAGCAAGGAGCACCACACTGAAAGTCGGGATCCTGCACCTGGTCAGAAGAGAGAAA 159
                                                                                                        GAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAG 311
                                                                                                                                                                         GAAGATCAGGGTGCAGCTGAGACTCAAGTGCCTGACCTGGAAGCTGATCTCCAGGAGCTG 219
                                                                                                                                                                                                                                                 312 GGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCG 371
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                                                                                                                                                                                                                                                                                                                                                                                      CCAAATCCAGAGGAGGTGAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAA 428
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NUMBER OF SEQ ID NOS: 140
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Pred. No. 9.6e-31;
0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09970607
GENERAL INFORMATION:
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Best Local Similarity 59.8
Matches 286; Conservative
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                                                                                                                                                                                     GCCAGGAACAGGGICACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG 360
                                                                                                                                                                                                                                        361 AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AGTGTTAAAAGAAGGCACGT----TGAAATGATGCAGGCTGCTCCTATGTTGGAAATT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTTTCAAGCAAGACAAATGAAGACTGAAACCAAGAACGTTATTCTTAATCTGGAAATT 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Addarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT PILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
RIOR FILING DATE: 2003-04-07
ROWBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
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Pred. No. 2.1e-29;
0; Mismatches 94.
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APPLICANT: Stache-Crain, Birgit
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Best Local Similarity 66.9
Matches 239; Conservative
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ORGANISM: Homo sapiens
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US-10-821-234-590
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LENGTH: 336
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD CURRENT APPLICATION NUMBER: US/10/453,372

CURRENT FILING DATE: 2003-06-03

PRIOR APPLICATION NUMBER: 09/789390

PRIOR APPLICATION NUMBER: 09/18930

PRIOR APPLICATION NUMBER: 09/18967

PRIOR APPLICATION NUMBER: 00/18567

PRIOR APPLICATION NUMBER: 00/18592

PRIOR FILING DATE: 2000-03-01

PRIOR PLING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-10

PRIOR PLING DATE: 2000-03-10

PRIOR PRIOR APPLICATION NUMBER: 09/833446

PRIOR FILING DATE: 2001-03-19

PRIOR PRIOR APPLICATION NUMBER: 09/833446

PRIOR PRIOR APPLICATION NUMBER: 09/83346

PRIOR PRIOR APPLICATION NUMBER: 09/93346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CATCTGTGTAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 120
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PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2001-06-24
PRIOR PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR PILING DATE: 2000-08-25
PRIOR PRIOR PRIOR DATE: 2000-08-25
PRIOR PRIOR DATE: 2001-08-25
PRIOR FILING DATE: 2001-08-25
PRIOR PRIOR SEQ ID NOS: 1609
SUPPRIARE: CLIRASeqList version 0.1
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Pred. No. 2.8e-26;
0; Mismatches 182;
Sequence 475, Application US/10453372 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/863776
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Matches 277; Conservative
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ORGANISM: Homo sapiens
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US-10-453-372-475
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LENGTH: 501
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CURRENT APPLICATION NUMBER: US/09/970,607
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/182,724
PRIOR FILING DATE: 2000-02-15
PRIOR PELING DATE: 2000-02-21
PRIOR APPLICATION NUMBER: 60/184,497
PRIOR PILING DATE: 2000-02-23
PRIOR PELING DATE: 2000-02-23
PRIOR PELING DATE: 2000-02-23
PRIOR PELING DATE: 2000-02-24
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349 TCAAGCAAGACAAATGAAGACTGAAACCAAGAACGTTATTCTTAATCTGGAAATTTGACT 408
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Pred. No. 4.4e-24;
0; Mismatches 174;
                                                                                                                                                                                                                                  434
                                                                                                                                                 480 ATTAAAATTCTCCCAATAAAGCTTTA
                                                                                                                                                                                                                                  409 GATAATATTCTCTTAATAAAGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 43, Application US/09970607; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.0%;
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US-09-970-607-43
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Best Local Similarity
Matches 254; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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18-09-370-6074

GENERAL INFORMATION:
APPLICANT: Malyankar et al.
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same;
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same;
CURRENT APPLICATION NUMBER: US/09/970,607
CURRENT FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 2000-02-23
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                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 57.8
Matches 258; Conservative
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US-09-970-607-44
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US-09-970-607-44
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426 TAAAAGAAGGCACGT----TGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTC 479
                                                            349 TCAAGCAAGACAAATGAAGACTGAAACCAAGAACGTTATTCTTAATCTGGAAATTTGACT 408
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PRIOR PLILING DATE: 2000-03-27

PRIOR PELING DATE: 2000-01-14

PRIOR PELING DATE: 2000-01-14

PRIOR PELING DATE: 1999-11-18

PRIOR PELING DATE: 1999-11-18

PRIOR PLING DATE: 1999-11-18

PRIOR PLING DATE: 1999-11-18

PRIOR PLING DATE: 1999-11-18

PRIOR PLING DATE: 1999-11-13

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-04-09

PRIOR PLING DATE: 1999-04-15

PRIOR PLING DATE: 1999-04-15

PRIOR PLING DATE: 1999-04-15

PRIOR PLING DATE: 1998-01-15

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PRIOR PLING DATE: 1998-07-13

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helper, William
APPLICANT: Helper, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.1%; Score 101.6; DB 5; Length 5 61.2%; Pred. No. 5.9e-21; Live 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/570,737A CURRENT FILING DATE: 2000-05-12
                                                                                                                                                                                   409 GATAATATTCTCTTAATAAGTTTTA 434
                                                                                                                         480 ATTAAAATTCTCCCAATAAAGCTTTA
                                                                                                                                                                                                                                                                                                                                         Sequence 472, Application US/09570737A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/568,100
PRIOR FILING DATE: 2000-05-09
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | LOCATION: (1)...(315)
| OTHER INFORMATION: n = A,T,C or
US-09-570-737A-472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.19
Best Local Similarity 61.29
Matches 221, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li, Samuel
                                                                                                                                                                                                                                                                               RESULT 12
US-09-570-737A-472
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APPLICANT:
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AND METHOL
241 CTCAGGAGGAGAGGATGAGGGAGCATCTGCAGGTCCAAGGGCCGAAGCCTGAAGCTGATA 300
                                                                                                                                                                                                                                                                                                                 301 GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAAGATGGTCCTGATGGCCAGG 360
                                                                                                                                                                                                                                                                                                                                                                                                    255 GCCAGGAAATGGATCTGGAAAAGACTCGGAGTGAGCGTGGAGGATGGCTCTGATGTAAAG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                         201 GACAAGAGAGAA-----GGAACACCTCCGATCGAAGAACGTAAAGTAGAAGGTGATT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AAGTTAAAAAGAAGAAGCTGAAGCTACACACATGGCTGATGTCACATTGAAAATGTGA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 AGARGACTCCACCTRATCCTRAGCATGCTAAGACTRAAGAAGCAGGAGATGGGCAGCCAT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
FILE REFERENCE: 21402-589
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILLING DATE: 2003-06-03

PRIOR FILLING DATE: 2003-06-03

PRIOR FILLING DATE: 2001-02-23

PRIOR FILLING DATE: 2001-02-23

PRIOR FILLING DATE: 2000-03-01

PRIOR PLICATION NUMBER: 09/89394

PRIOR PLICATION NUMBER: 09/893187

PRIOR PLING DATE: 2001-03-29

PRIOR PLING DATE: 2001-03-10

PRIOR PLING DATE: 2001-03-10

PRIOR PLING DATE: 2001-03-10

PRIOR PLING DATE: 2001-03-10

PRIOR PLING DATE: 2001-03-10

PRIOR PLING DATE: 2001-03-25

PRIOR FILLING DATE: 2001-05-23

PRIOR PLING DATE: 2001-05-23

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2000-06-21

PRIOR PLING DATE: 2000-06-25

PRIOR PLING DATE: 2000-06-25

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2000-06-25

PRIOR PLING DATE: 2000-06-25

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2001-06-24

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-06-25

PRIOR PLING DATE: 2001-06-25

PRIOR PLING PRIOR APPLICATION NUMBER: 60/227800

PRIOR PLING PRIOR APPLICATION NUMBER: 60/227800

PRIOR PLING PRIOR APPLICATION NUMBER: 60/227800

PRIOR PLING PRIOR APPLICATION NUMBER: 60/227800

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 477, Application US/10453372 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 213; Conserv
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; LOCATION: (23)
US-10-453-372-477
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US-10-453-372-477
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APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
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                                                                                                                                                                                         GGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAA 308
                                                                                                                                                                                                                                                                                                                                                                CAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGAC 368
                                                                                              103 GAAAAACGICAAGAAGAAGCACCACCAACIGATAATCAGGGTATTGCACCTAGTGGGGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 GGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTGATAGCCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 ATCGAAATGAAGGAGCACCTGCCGTTCAAGGGCCTGACATGGAAGCTTTTCAACAGGAA
                                                                                                                                                                                                                                                                               163 ATCGAAAATGAAGGAGCACCTGCCGTTCAAGGGCCTGACATGGAAGCTTTTCAACAGGAA
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                      GCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 ATGCCCACTTTTGATCTCACTAAAGTGCTGGAAGCAGGTGATGCGCAACCATAGT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Pred. No. 1.9e-19;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANI: ALBODIOM. THERAPEDTIC POLYPEPTIDES, TILL REFRENCR: 21402-589 A
CURRENT APPLICATION NUMBER: 05/0453,372
CURRENT FILING DATE: 2003-06-03
REIOR APPLICATION NUMBER: 09/789390
PRIOR APPLICATION NUMBER: 60/18930
REIOR APPLICATION NUMBER: 60/18967
REIOR PILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR APPLICATION NUMBER: 60/195792
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-06-23
PRIOR FILING DATE: 2001-06-23
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PRIOR FILING DATE: 2001-06-23
PRIOR FILING DATE: 2001-06-23
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Best Local Similarity 63.2%;
Matches 148; Conservative
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ORGANISM: Homo sapiens
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US-10-453-372-487
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NAME/KEY:
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                                    189
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CURRENT APPLICATION NUMBER: 09/789390

PRIOR FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 60/185967

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR PLILOR DATE: 2000-03-10

PRIOR PLILOR DATE: 2000-03-10

PRIOR PLILOR DATE: 2000-03-19

PRIOR PLILOR DATE: 2000-03-19

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7, 2004, 11:07:15; Search time 3602 Seconds (without alignments) 6485.812 Million cell updates/sec OM nucleic - nucleic search, using sw model US-09-782-745-18 August Title: Perfect score: Scoring table: Sequence: on: Run

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KEYWORDS)			
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ORGANISM	Unknown.						
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ALIGNMENTS

REFERENCE AUTHORS TITLE

Unclassified.

1 (bases 1 to 539)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and Boon-Falleur,T.
Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof

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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Buggen, P. V. D., Eynde, B. V. D., Debacker, O. and Falleur, T. B.

Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof patent: JP 2002509859-A 11 02-AR-2002;

LUDMIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapinas (human)

PN JP 2002509859-A/11

DD 02-AR-2002

PF 12-AN-1999 JP 200528886

PR 23-JAN-1999 US 09/012818

PI PIERRE VAN DER BRUGGEN, BENOIT VAN DEN EYNDE, OLIVIER DEBACKER, PI THIERRY BOON FALLEUR
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             Location/Qualifiers
                                   /organism="unknown"
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                                                                                   100.0%;
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JP 2002509859-A/11.
Homo sapiens (human)
Homo sapiens
                                                                                                    Best Local Similarity 100.
Matches 539; Conservative
                         1. .539
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1 (bases 1 to 539)
Van den Bynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and their
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Location/Qualifiers
PC C07K4/12,C12N15/09,C12P21/00,C12Q1/02,C12N15/00
Strandedness: Single;
CC Topology: Linear;
CC STRANDEDNESS:single,TOPOLOGY:linear
FF Key Location/Qualifiers
Location/Qualifiers
//organism='Homo sapiens (human)'
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100.0%; Pred. No. 3.2e-128;
iive 0; Mismatches 0;
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Sequence 18 from patent US 5648226.
                                                                                                                                                 1. .539
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DEFINITION

RESULT 4 BD132471

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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29-SEP-1999
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Isolated peptides derived from the gage tumor rejection antigen
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van der Bruggen,P., van den Bynde,B., DeBacker,O. and
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Pred. No. 3.2e-128;
Mismatches 0;
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llarity 99.4%; Pred. No. 3.6e-125;
Conservative 0; Mismatches 3;
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Patent: US 5858689-A 17 12-JAN-1999;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 17 from patent US 5858689.
     /mol_type="genomic DNA"
/db xref="taxon:32630"
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Conservative 0;
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NCE 1 (bases 1 to 539)
DAS Debacker, O., Eynde, B.V.D. and Falleur, T.B.
Is Oblated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof LUDWIG INSTITUTE FOR CANCER RESEARCH
PA DP 2002507112-A.11
PD 05-MAR-2002;
PR 23-UNN-1997 JP 1998503430
PR 24-JUN-1996 US 08/659161
PI OLIVIER DEBACKER, BENOIT VAN DEN EYNDE, THIERRY BOON FALLEUR PC Strandedness: Single, Incation/Courter.
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                                                   539; DB 6; I
No. 3.2e-128;
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/mol_type="unassigned DNA
                                                 Score Pred.
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JP 2002507112-A/11.
                                                 100.0%;
al Similarity 100.0%;
539; Conservative 0
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                          Score 527.2; DB 6;
Pred. No. 3.6e-125;
0; Mismatches 3;
                             97.8%;
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E 2 (Dasses 2 modelae; Daylor, Debacker, O. and Falleur, T.B.

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                                                                   CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC 127
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/mol_type="genomic DNA"
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368 AGGIGGACCCGCCAAAICCAGAGGAGGIGAAAACGCCIGAAGAAGGIGAAAAGCAAICAC
                                                                                      428 AGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
                                                                                                                                     AGIGITAAAAGAAGGCACGTIGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
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Van den Bynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and
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larity 99.4%; Pred. No. 3.6e-125;
Conservative 0; Mismatches 3;
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Location/Qualifiers
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Sequence 17 from patent US 5648226.
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/mol_type="unassigned DNA"
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Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
1. 527
/organism="Homo. sapiens"
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                                                                               GCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
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/db_xref="GI:914909"
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1 (bases 1 to 532)
Debacker,O., Ende,B.V.D. and Falleur,T.B.
Isolated, nucleic acid molecules which code for GAGE tumor rejection antigen, the tumor rejection antigen, and uses thereof pattent: 19 2002507112-A 10 05-MAR-2002,
DIUDWIG INSTITUTE FOR CANCER RESEARCH
PN JP 2002507112-A/10
PP 05-MAR-2002
PP 23-JUN-1997 JP 1998503430
PR 24-JUN-1996 US 08/669161
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                                          GCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
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Pred. No. 3.6e-125;
0; Mismatches 3;
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Matches 529; Conservative C
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2 (bases 1 to 528)
Van Den Eynde, B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EXNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
2 GCCAGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTAC
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1 (bases 1 to 528)
Van den Bynde, B., Peeters, O., De Backer, O., Gaugler, B.,
and Boon, T.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="adult"
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/cell_line="MZ2-MEL.43"
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Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 4e-125;
); Mismatches 0;
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99.4%; Pred. No. 6.9e-124;
live 0; Mismatches 3;
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Direct Submission

Submitted (28-DEC-1994) BENOIT J VAN DEN EXNDE, Ludwig Institute
Submitted (28-DEC-1994) Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
         /translation="MSWRGRSTYYWPRPRRYVQPPEMIGPMRPEQFSDEVEPATPEEG
EPATQRQDPAAAQEGEDEGASAGQGPRPEADSQEQGHPQTGCECEDGPDGQEMDPPNP
EEVKTPEEGEKQSQC"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                  Gaps
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                                                                                Score 522.2; DB 9;
Pred. No. 6.9e-124;
0; Mismatches 3;
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xref="GI:914905
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                                                                                  Query Match 96.9%;
Best Local Similarity 99.4%;
Matches 524; Conservative
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/trānslation="MSWRGRSTYYWPRPRRYVOPPEVIGPMRPEQFSDEVEPATFEEG
EPATQRQDPAAAQEGEDEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNP
EEVKTPEEGEKQSQC"
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1 (bases 1 to 524)
Chen,M.E., Lin,S.-H., Chung,L.W.K. and Sikes,R.A.
Isolation and characterization of PAGB-1 and GAGB-7: new genes expressed in the LNCaP prostate cancer progression model that share
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Homo sapiens melanoma antigen related GAGE-7 mRNA,
AF058998
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
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                                                                                                                                                                                         /codon_start=1
/product="GAGE-5 protein"
                                                                                                                                                                                                                                                 /protein_id="AAA82748.1"
/db_xref="GI:914907"
                                                                                                       /tissue_type="melanoma"
/dev_stage="adult"
75. .428
                                                                                      cell line="MZ2-MEL.43"
mol_type="mRNA"
db_xref="taxon:9606"
                                                             sex="female"
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Homo sapiens
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5858689
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Sequence 14 from patent
AR028488
AR028488.1 GI:5940461
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Best Local Similarity 98.0%;
Matches 528; Conservative
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Homo sapiens (human)
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EPATQRODPAAAQEGEDBGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNP
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/note="similar to GAGE family of melanoma antigens"
                J. Biol. Chem. (1998) In press
2 (bases 1 to 524)
2 (bases 1 to 524)
Direct Submission. H., Chung, L.W.K. and Sikes, R.A.
Direct Submission. Chung, L.W.K. and Sikes, R.A.
Submitted (07-APR-1998) Urology, University of Virginia,
Charlottesville, VA 22908, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                       524;
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product="melanoma antigen related GAGE-7"
protein_id="AAC25989.1"
db_xref="G1:3300090"
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 515.2; DB 9;
Pred. No. 4.4e-122;
2; Mismatches 5;
  homology with melanoma associated antigens
                                                                                                                                   organism="Homo sapiens"
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Matches 517; Conservative
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PAT 29-SEP-1999

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Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof. BD231797. BD231797.1 GI:33041567
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 538)
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                                                                             Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
Patent: US 5858689-A 14 12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCAGGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTAC
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1 (bases 1 to 538)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and
Boon-Falleur,T.
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                  DB 6;
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Bruggen, P.V.D., Eynde, B.V.D., Debacker, O. and Falleur, T.B.
Isolated polypeptides binding with HLA-A29 molecule, nucleic acids as molecules encoding the same, and utilization thereof.

ALCONOMICAL STRUTUTE FOR CANCER RESEARCH
OS Home sapiens (human)
PN JP 2002509859-A/7

BD 02-APR-2002

PF 12-JAN-1999 UP 2000528586

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGT 180
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Pred. No. 8.7e-121;
0; Mismatches 8;
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BM836021 BU533718 CE7847043 CE150355 CE150355 CE150355 CE150355 BG181480 BG181480 BG184057 BG1860 BG12621 BG212621 BG212621

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AA868226 AA448542 BM836228 BC005363

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GenCore (c) 1993 -

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BM832793 K-EST0107
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BM832793 537 bp mRNA linear EST 06-MAR-2002 K-EST0107334 S5SNU484s1 Homo sapiens cDNA clone S5SNU484s1-8-F10 5', mRNA sequence.	BM32793.1 GI:19189202 EST. Homo sapiens (human) Homo sapiens (chuman) Estkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 537) Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S. 21C Frontier Korean EST Project 2001	, & Biotechnology 333, South Korea
537 bp mRN omo sapiens c	nta, Craniata es; Catarrhi	., Lee,J.Y., n,H.Y., Kim,C	of Bioscience Daejeon 305- Daej
		(hoses 1 to 537) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y. Kim,Y.G., Cheong,J.E., Sohn,H.Y., Kim Kim,Y.S. 21C Frontier Korean EST Project 2001	Onpublished Contact: Kim YS Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology Korea Research Institute of Bioscience & Biotechnology 52 Eceun-Gong Yusecong-guu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Bmail: yongsmail.kribb.re.kr Plate: 8 row: F column: 10 High quality sequence stop: 537.
RESULT 1 BM832793 LOCUS DEFINITION	YERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	COMMENT

ALIGNMENTS

AA972716 BG216461 AF318372 AA738394 CB961487

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this is a NIH MGC Library."
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Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Homo sapiens"
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Best Local Similarity 97.9%;
Matches 516; Conservative
                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                       mRNA sequence.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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KEYWORDS
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/competent cells E. coli DNA ligase after digestion of competent cells E. coli Top10f" by alectroporation method. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription resion when the synthesis of biotinylated single stranded RNA by in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with aridin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120
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Pred. No. 2.8e-98;
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location/Qualifiers
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Best Local Simil
Matches 534; C
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                      Source
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EST 04-OCT-2001
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/lab host="DH10B"
/clone_lib="NHH MGC 119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Not1;
/note: anotymous male age 7. Library is oligo-dT primed and directionally cloned (BCoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full:length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó,
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                                                                                                                                                                                                                                                                    BI826605 527 bp mRNA linear EST 04-OCT-200
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11419 row: p column: 13
High quality sequence stop: 519.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCCGAGCAGTTCAGTGATGAAGTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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.2e-93;
.es 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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Gaps

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257 240 317 360

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Contract: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Genomics
National Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RM10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov.
Tissue Procurement: James Martin, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M. A.G.E. Consoration
Clone distribution: MGC clone distribution information can be found through the I.M. A.G.E. Consortium/LLNL at:
Plate: NDAM604 row: e column: 12
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AACACCTGAAGAGAGGAGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGG
                                                                                                                             PTCCTCTACTGAGATTCATCTGTGTG
                                                                                                                                                                            1 CAGIGCIGIGIGGIICCIGCCGICCGGACTCITITICCICTACTGAGAIICAICIGIGIG
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National Institutes of Health, Mammalian Gene Collection (MGC)
                 DB 13; Length
                                                                      Indels
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              Score 508.8; DB 13;
Pred. No. 1.6e-93;
0; Mismatches 7;
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Location/Qualifiers
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           94.4%;
98.7%;
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Homo sapiens
           Query Match
Best Local Similarity 98.7
Matches 513; Conservative
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DEFINITION
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JOURNAL
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KEYWORDS
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CF780547
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/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/done="lMAGB98R213161; IMAGE:1256204"
/tissue_type="poloded germ cell tumors"
/tishost="mrloded germ cell tumors"
/tlone=lnbent="mrloded germ cell tumors"
/tlone=lnbentcor: privide GOAP GO3"
/clone=lnbentcor: privide GOAP GO3"
/note="Westor: privide GDAP was prepared from 3 pooled germ cell tumors, and was then primed with a Not I olyplinker; 1st strand cDAP was prepared from 3 pooled germ cell tumors, and was then primed with a Not I olyplinker; 1st strand coloned stranded cDAP was ligated to coling off) primer. Double-stranded cDAP was ligated to CO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified privided into the Not I and Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-FEB-2003
                                           CAGGAGGAGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGC 300
                                                                                                                                                       370 GTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAG 429
                                                                                                                                                                                                                                                                         361 ATGGACCGGCCAAATCCAGAGGAGGAGAAACGCCTGAAGAAGGTGAAAAGCAATCACAG 420
                                                                                                                                                                                                                                                                                                                                               489
           309
                                                                                                                                                                                                                                                                                                                                                                                           421 IGITAAAAGAAGGCACGIIGAAAIGAIGCAGGCIGCTCCIAIGIIGGAAAITIIGIICATI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DALUGZZ/ SZI DD MRNA linear EST 06-FEB-2
BX108227 NCI_CGAP_GC3 Homo sapiens CDNA clone IMAGp998K213161 ;
BX108377 NCI_CGAP_GC3 Homo sapiens CDNA clone IMAGp998K213161 ;
PX108377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neubert, P., Partsch, E., Peters, M.,
CAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGC
                                                                                                              CAGGAACAGGGTCACCCACAGACTGGGTGTGTGAAGATGGTCCTGATGGCAGGAG
                                                                                                                                                                                                                                                                                                                                      TGTTAAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RZPDLIB; I.W.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
Http://www.zzpd.de/CloneCards/Cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GmbH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 521)
Ebert,L., Heil,O., Hennig,S., Neubert
Radelof,U., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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DEFINITION
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BX108227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="adenocarcinoma, cell line"
/lab.host="DH10B (phage-resistant)"
/clone lib="NIH MGC 90"
/note="organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                            Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                      Context: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM12026 row: 1 column: 24
High quality sequence stop: 509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
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                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoo Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 509)

NIH-MGSChttp://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5402663"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGTTCATTAAATTCTCCCAA 502
                     sapiens (human)
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Matches 49
                                              ORGANISM
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                                                                                                                                                          /clone_lib="NIH_MGC_217".
/note="Vector: pYx-Agc; Site_1: EcoRI; Site_2: NotI;
/note="Vector: pYx-Agc; Site_1: EcoRI; Site_2: NotI;
Library is oligo-dT primed and directionally cloned
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cNNA synthesis was primed with oligo-dT
Primer containing a Not I site. Double strand cDNA was
size selected according tomRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI868671 509 bp mRNA linear EST 11-OCT-2001 603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5',
                                                                                                                                                                                                                                                                                                                                       directionally into pXX.Asc vector. Average insert size
0.5-1Kb. Adaptors 5. (AATTCGGCACGAGS)3, and 5.4
(CCTCGTGCGG)3. 3' Linker sequence - GCGGCCGTGAGAGC T18.
Sequencing primers 3'end: T3 promoter primer 5'd
(ATTAACCGTCACTAAAGGGA)3'. 5' End: T7 promoter primer 5'd
ATATACGACTACACTAGGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library."
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                                                                                                                Tumor cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 503.4; DB 14; Length 517; Pred. No. 2e-92; 0; Mismatches 6; Indels 0;
                                                                                        /clone="IMAGE:30524555"
/tissue_type="Pooled Chondrosarcoma Tu
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTCTCCCAATAAAGCTTTACAGCCTTCTGCA 516
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                            /organism="Homo sapiens"
/mol_type="mRNA"
                                                                      db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI868671.1 GI:16042344
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98.8%;
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Length Indels 127

180 187 240 247 307 360 367 420

120

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_Arsf="texaon:9606"
/clone="InAGE:2911881"
/lab_host="DH108"
/clone lib="Soares NFL T GBC S1"
/note="Corgan: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Bco RI; Bqual amounts of plasmid DNA from three normalized libraries (fetal lung NbH119W, testis NHT, and B-cell libraries (fetal lung NbH119W, testis NHT, and B-cell vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW510753 457 bp mRNA linear EST 03-MAR-2000 hd39d05.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2911881 3' similar to SW:GGB4_HUMAN Q13068 GAGE-4 PROTEIN. ;,
                                                                                                                                                                               400
                                                                                                                                                                                                          250 Grchadgeccanagecrenagecrenagecandancagecrenecencagecregeries 191
                                                                                                                                                                                                                                                                        401 CGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAG 460
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (Dases 1 to 457)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                     70 GCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAAGCTTTACAGCCTTC
                                     281 GTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCCACAGACTGGGTGTG
                                                                                                                                                                            341 AGTGTGAAGATGGTCCTGATGGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAA
                                                                                                                                                                                                                                                                                                                                                                   461 GCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTC
            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW510753.1 GI:7148831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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Best Local Simi
Matches 453;
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                                  310
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/clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clottech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified py773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                          489 bp mRNA linear EST 04-JUN-1997 Soares testis NHT Homo sapiens cDNA clone IMAGE:782636 to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 CAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCAG 280
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 489)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Mhore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGACTCTTTTCCTCTACTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGAT
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H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 471.6; DB 9; Length 489;
Pred. No. 6.1e-86;
0; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'lab host="DH10B"
                                                                                                                                                                                                                                                              GI:2161229
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                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Best Local Similarity 99.0
Matches 485; Conservative
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                                                                                                                                                                     zw81e11.s1
3' similar
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                  germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded CDNA was ligated to Ec
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
polylinker; 1st strand cDNA was prepared from 3 pooled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1381509 447 bp mRNA linear EST 28-MAR-te76b07.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2092597 3' Similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
                                                                                                                                                                                                                                                                                                                                                                                                    ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCT
                                                                                                                                                                                                                                                                                                                               164 Argagiriegecgaggaagarcgaccrerrarregecragiccaagacgerargracageer
                                                                                                                                                                                                                                                                                                                                                                             CCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAG
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                                                                                                                                                                                                Length 464;
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Pred. No. 6.5e-80;
0; Mismatches 10;
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AI381509
AI381509.1 GI:4194290
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97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                              Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTIEST. NCI CGAP GC3 Homo sapiens CDNA clone IMAGE:1256204 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN.; mRNA sequence. AA738037.1 GI:2768794
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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/tissue type="pooled germ cell tumors"
/lab host="mollDB"
/clone lib="NCI CGAP GC3"
/note="Vector: pI773D-Pac (Pharmacia) with a modified
                                                                                                                315 ACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGCAGGAGGTGGA
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                                                                                           <u> ACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Bomail: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.
Bommert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Library Preparation: Most CGAP Clone distribution infort found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 511 Std Error: 0.00
Seq primer: -doml3 fwd. FT from Amersham
High quality sequence stop: 435.
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/db_xref="taxon:9606"
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CB115693 505 bp mRNA linear EST 28-JAN-2003 K-EST0159805 L8SCKO Homo sapiens cDNA clone L8SCKO-8-B09 5', mRNA
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                                                                                                                                                                                                                                                                                                                                       /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_90"
/note="Grgan: liver, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size_1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can h
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAMI0239 row, p column: 07
High quality sequence stop: 480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.1%; Score 437; DB 12; Length 480; ilarity 98.9%; Pred. No. 6.8e-79; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                          clone="IMAGE:4451958"
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                                                                           /done libe-Soares NFL T GBC S1"
/done libe-Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087; 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:2092597"
/lab_host="DH10B"
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                                                  Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Xim. M. R.
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                                                                                                  21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 436; DB 14; Length 505; Pred. No. 1.1e-78;
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/organism="Homo sapiens"
                                                                                                                                                                                                                    Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 8 row: B column: 09
High quality sequence stop: 505.
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/db_xref="taxon:9606"
/clone="L8SCK0-8-B09"
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RESULT

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
CDMA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Worl-CAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llhl.gov/bbrp/lange/limage.html
Seq primer: -40ml3 fwd. Ef from Amersham
High quality sequence stops: 331.
nx32b08.sl NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1257855 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 450 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 4e-78;
0; Mismatches 4; Indels 1
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/lab_host="DH10B"
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/mol_type="mRNA"
/db xxef="taxon:9606"
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/dlone="ITMAGE:271986"
/lab host="DH108 (Life Technologies)"
/dlone="ITMAGE:271986"
/dlone="ITMAGE:271986"
/dlone="Ithe"NOI CGAP Sub2"
/dlone="Vector: pT773D-pec (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The
NOI CGAP Sub2 library is a subtracted library derived from
BI. B constitutes a mixture of 21 normalized or
Subtracted NOI CGAP libraries: NOI CGAP CO4,
NOI CGAP Pr22, NOI CGAP Fx18, NOI CGAP Fx112,
NOI CGAP Kid3, NOI CGAP Kid11, NOI CGAP Kid12,
NOI CGAP Ex2, NOI CGAP Kid11, NOI CGAP Ex11, NOI CGAP Lei2,
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. CDNA Librarian information: M.B. Soares Lab Clone distribution:
NCT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at:
www-bio.lln.gov/bbrp/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 bp mRNA linear EST 10-SEP-1999 UI-H-BIOp-abg-g-06-0-UI.sl NCI_CGAP_Sub2 Homo sapiens CDNA clone IMAGE:2711986 3', mRNA sequence.
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                                                                                                                                                                                                                                                277 GATGAGGGAGCATCTGCAGGTCAAGGCCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGT 218
                                                                                                                                      AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAG 441
       CCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 ACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTTCTCCCA 501
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                      GATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone lib="Soares testis_NHT"
/note="Vector: pTyT3D-Pac T(Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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Insert Length: 504 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 10-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           AI187350 455 bp mRNA linear EST 10-NOV-1996 gf29a05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1751408 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 CCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACA 201
                                                                      501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                  31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
       91
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
150 AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAG
                                                               442 ACACGITGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCA
                                                                                                                                  90 ACACGITGAAAIGAIGCAGGCIGCICCIAIGIIGGAAAITIGIICAIIAAAAIICICCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455 ATGAGTTGGCGAGGAAGATGACCTTATTATTGGCCTAGA-CAAGGCGCTATGT-CAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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Pred. No. 3.8e-75;
0; Mismatches 9; Indels 2
                                                                                                                                                                                                     502 ATAAAGCTTTACAGCCTTCTGCAAAAAAA 532
                                                                                                                                                                                                                                            ATAAAG-TTTACAGCCTTCTGCAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1751408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seg primer: -40UP from Gibco
High quality sequence stop: 391
Location/Qualifiers
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446; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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AI187350.1
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AI187350/c
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VERSION
KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
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ð CP à M. Fatima

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
/clone_lib="Soares testis NHT"
/clone_lib="Soares Taylo-pac"(Pharmacia) with a modified
/note="Vector: pT/71D-pac"(Pharmacia) with a modified
polylinker; Site_1: Not_1; Site_2: Eco_RI; 1st_strand_cDNA
was prepared from mRNA obtained—from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGAAGCCTGAAGCTGATAGCCAGGACAGGGTCACCCACAGACTGGGTGTGAGTGTGAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGGTCCTGATGGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGTCCTGATGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4946)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTGGCCTAGACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 TATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGNANTTGCCTATGCGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAACTTTACAGCCTTCTTCAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one round of normalization to Cots, and
by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                        Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 Ww. BT from Amersham High quality sequence stop: 363.
Location/Qualifiers
                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels
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Pred. No. 8.7e-71;
0; Mismatches 15;
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1409245"
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96.4%;
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Unpublished (1997)
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                                                                    in a subtractive hybridization with a driver whose composition is detailed below: NCI CGAP Kid3 pool 1 LLAM 3334-3337, 362-3683, 3798-398 [IMAGE CloneIDS 1322376-132391], 1456008-1456775, 1500552-150285)
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDS 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI CGAP LUS pool 1 LLAM 3575-3582, 1492104-1493255) NCI CGAP LUS pool 1 LLAM 3575-3582, 1492104-1493255) NCI CGAP LUS pool 1 LLAM 3575-3582, 1500904-1522439) NCI CGAP LUS pool 1 LLAM 3575-3582, 1500904-1522439) NCI CGAP CONCIDS 1257096-1258631, 1469064-1470993, 1475592-1476743) NCI CGAP PT22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 1267066-1258631, 1469064-1470993, 1475592-1476743) NCI CGAP PT22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 1057416-1061255, 1144584-1145351) The resulting subtracted library contained 4 million recombinants. Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. TAG_INB-NCI CGAP_GC4
TAG_INB-NCI CGAP_GC4
TAG_INB-NCI CGAP_GC4
TAG_INB-NCI CGAP_GC4
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NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25.
These 21 libraries were pooled and a single-stranded DNA
preparation of the resulting mixture was used as a tracer
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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N_Geneseq_29Jan04:* .: geneseqn1980s:* : geneseqn1990s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2000s:* 55: 77: 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

Aas60496 Human can Abz1955 Group III Abz1955 Group III Abz20497 TPG1 subt Abz18686 Group III Abz18791 Group III Abz18791 Group III Abz18791 Group III Abz18731 Human can Lung canc CDNA enco GAGE-2 tu Human GAG Human GAG GAGE-2 fu Human sec Human can Aax18721 cDNA enco Aax90522 GAGE-5 tu Acc51027 Human bla Lung canc Description Abx76236 Ab166323 Aav18720 Ada15802 Ada15801 Ada15801 Ab220463 Aav18717 Aac02129 | Aas60104 | SUMMARIES ABX76236 ABL66323 AAV18720 AAX90519 ADA15802 ADA15801 AAS60496 ABZ19551 ABZ19755 ABZ20497 ABZ20480 ABZ18686 ABZ18686 ABZ18737 ABZ185737 AAV18717 AAC02129 AAS60104 AAV18721 AAX90522 ABZ20463 ACC51027 Length DB 4430 2530 2277 2227 2229 2229 2259 Query 4444455.3 4425.0 4425.0 4425.0 4426.0 4466.0 93.2 66.1 56.2 55.8 529.4 527.2 527.2 527.2 5527 510.2 510.2 502.8 502.8 502.8 368.4 368.4 300.8 227 226 218.4 210 204 Score 244 242.4 242.4 227.4 Result No. ט ט υυυυ

Abx77605 Different	Acd42232 Human GAG	Adc24646 Human cDN	Aai60530 Human pol	Abz19538 Group III	Aas69484 DNA encod	Abt15728 Human can	Aad14981 Human NOV	Abt15736 Human can	Aaf68151 Human lun	Abk38062 cDNA enco	Acal0391 Human lun	Abx99342 Lung canc	Ade72125 Human lun	Aad24228 Human dif	Aba92217 Melanoma	Aah93807 Human pro	Aas63900 Human pro	Aah02872 Prostate	Aah85121 Human pro	Aca59708 Prostate	Ab195271 Human P10
ABX77605	ACD42232	ADC24646	AAI60530	ABZ19538	AAS69484	ABT15728	AAD14981	ABT15736	AAF68151	ABK38062	ACA10391	ABX99342	D ADE72125	AAD24228	ABA92217	AAH93807	AAS63900	AAH02872	AAH85121	ACA59708	ABL95271
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202.4	202.4	202.4	187	178	164.2	144.8	134.8	129.8	109.6	109.6	109.6	109.6	109.6	105.2	105	103.2	103.2	103.2	103.2	103.2	103.2
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen, cytolytic T cell clone proliferation; HIA-typing assay; ss.
                                                                                                                                                                                                                                                                                                                                         tumour rejection antigen precursor peptides, useful to diagnose
                                                               cDNA encoding GAGE-6 tumour rejection antigen precursor.
                                                                                                                                                                aa:Arg)
aa:Ala)
aa:Thr)
                                                                                                                                                               (pos:127. .129, e (pos:196. .198, e (pos:199. .201, e
                                                                                                                                                                                                                                                                                             Van Den Eynde B, Boon-Falleur T;
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          BP
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          AAV18721 standard; cDNA; 539
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                                                                                                                                                                                                                                                          96US-00669161.
                                            (first entry)
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                                                                                                                     sapiens
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                                            30-JUL-1998
                                                                                                                                                                                                                      31-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                            melanomas
                            AAV18721;
                                                                                                                                      Key
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The present sequence encodes a GAGE-6 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In

Example 13; Fig 4; 60pp; English.

98US-00012818. 99WO-US000775.

WO9937665-A1

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contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 14 Jasses located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE copys for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies.
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Pred. No. 7.1e-139;
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Human leukocyte antigen, HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte;
                                                                                          GAGE-5 tumour rejection antigen clone nucleotide sequence.
                        BP.
                        CDNA; 532
                                                                     entry)
                                                                   (first
                      AAX90522 standard;
                                                                                                                                                               sapiens.
                                                                    30~SEP-1999
                                             AAX90522
                                                                                                                                        GAGE: SS
                                                                                                                                                               Ношо
RESULT 2
           AAX90522
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532

TTABABATTCTCCCABTABAGCTTTBCBGCCTTCTGCBABABABABABA

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                                                                                                                                                                                                                                                                                                                                The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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Pred. No. 2.9e-138;
0; Mismatches 3;
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                                                                                                                                                                          Van Den Eynde
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                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
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529; Conserv
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GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAG 420
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                                                     GCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAA
                                                                                                              GCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGAT
                 GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAAACGTCAGGATCCT
GATGAAGTGGAACCAGCAACACTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
                                                                               GCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA
                                                                                                                                         GCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGGTGGATGGTCCTGAT
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                                                                                                                                                                                                                               CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
                                                                                                                                                                                                                                                                                      TIGITCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA 527
                                                                                                                                                                                                                                                                                                       TIGHTHAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer-associated polynucleotide #105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 273; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002WO-US012476.
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2001US-0339245P.
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2001US-0334370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-0372246P
                                                                                                                                                                                                                                                                                                                                                                                      ABX76236 standard; DNA; 527
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABU56512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200286443-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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29-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-2003
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                                                                                                                                                                                                                                                          421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for detecting a bladder cancer-
associated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with a polymucleotide
that selectively hybridises to a sequence that is 80 % identical to a
table of sequences (see ACC50951 to ACC50951 to ACC501059
encode the human bladder cancer-associated proteins given in ABR48146 to
ABR48242). Bladder cancer-associated sequences from the present invention
have cytoscatic activities, and can be used in antisense gene therapy and
in vaccine production. The method can be used for detecting a bladder
cancer-associated transcript in a cell from a patient. The method is
useful in diagnosing or treating bladder cancer and in screening for
compounds that modulate bladder cancer, such as hormones or antibodies.
The nucleic acid molecules from the present invention may be used in
various screening and diagnostic methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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                                                                                                                                           SS.
                                                                                                                                      Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                        Human bladder cancer associated cDNA sequence SEQ ID NO:144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 527; DB 7; Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 527 BP; 146 A; 113 C; 157 G; 111 T; 0'U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 279; 307pp; English
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100.08;
1°,
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666P.
                      ACC51027 standard; cDNA; 527
                                                                                                                                                                                                                                                       2002WO-US021338
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                                                                                                                                                                                              WO2003003906-A2.
                                                                                                                                                                                                                                                    03-JUL-2002;
                                                                                                                                                                   Homo sapiens.
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Lung cancer-associated polynucleotide, gene, ds, cytostatic, emphysema, antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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Homo sapiens.
gene;
administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polymuclectides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polymuclectides of the
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                  compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by
                   increased or decreased expression in lung cancer samples. Lung cancerassociated polynucleotides and polypeptides are used for identifying a
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at least 80 % identical to a gene that exhibits
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Best Local Similarity 100.
Matches 527; Conservative
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agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for anti-neoplastic agent involves exposing cells to a chemical
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20-SEP-2000; 2000US-0234034P.
20-SEP-2000; 2000US-0234034P.
20-SEP-2000; 2000US-023455P.
22-SEP-2000; 2000US-0234569P.
25-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234567P.
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2000US-0236033P.
2000US-0236034P.
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25-SEP-2000; 2000US-02350B2P.
25-SEP-2000; 2000US-0233134P.
25-SEP-2000; 2000US-0235134P.
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26-SEP-2000; 2000US-0235638P.
27-SEP-2000; 2000US-0235711P.
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27-SEP-2000; 2000US-0235840P.
27-SEP-2000; 2000US-0235863P.
28-SEP-2000; 2000US-0236028P.
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WO200194629-A2
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activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such properties of the agent, MI can be used in the treatment of cancer such prostate or branch, lung, thyroid, oesophageal, ovarian, kidney, prostate or panormeatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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                                                                                                                                                                                      Sequence 528 BP; 147 A; 114 C; 156 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                           Score 522.2; DB 6;
Pred. No. 7.5e-137;
0; Mismatches 3;
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                                                                                                                                                                                                                           tch 96.9%; al Similarity 99.4%; 524; Conservative
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Best Local Similarity
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The present sequence encodes a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CNAS for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for,

Isolated nucleic acid encoding GAGE tumour rejection antigen precursor processed by HLA-Cw6 molecules into peptides, useful to diagnose

Example 13; Fig 4; 60pp; English.

Boon-Falleur T;

m,

Van Den Eynde

Debacker O,

WPI; 1998-076905/07. P-PSDB; AAW47602

(LUDW-) LUDWIG INST CANCER RES

97WO-US010850 96US-00669161

23-JUN-1997; 24-JUN-1996;

WO9749417-A1 31-DEC-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TGGAACCAGAGCCTCCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GGTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.3%; Score 519.2; DB 2; 98.5%; Pred. No. 5.3e-136; ive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 98.5
les 524; Conservative
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240 307 367

GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay; ss.

Location/Qualifiers 75. .429 /*tag= a

Homo sapiens

Key

cDNA encoding GAGE-5 tumour rejection antigen precursor,

(first entry)

30-JUL-1998

AAV18720;

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The invention relates to isolated GACE-7B and GAGE-8 polypeptides and the nucleic acid molecules encoding them. The invention also relates to an
                                                                                                                                                                           New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tume rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, GAGE-7B; gene; ss; cytolytic T lymphocyte; CTL;
human leukocyte antigen, HLA; tumour rejection antigen precursor;
major histocompatibility complex; MHC; cytolytic T cell proliferation;
chromosome Xp11.2-p11.4.
                                                                                                                                                                                                                                                                                                      gcagcrigcricaggagagagagargaggagagagcarcrigcaggricaagggccgaagccrigaa
                                                                                                                                              GCTGATAGCCAGGAACAGGGTCACCACACACAGACTGGGTGTGAGTGTGAAGATGGTCCTGAT
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aa: HPQTGKPEAHSQEQ)
            GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
                                          GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
                                                                             GCAGCTGCTCAGGAGGAGAGAGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA
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ccept= (pos:115.
ccept= (pos:265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA15802 standard; cDNA; 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human GAGE-7B cDNA.
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                                                                                                                                                                                                                                                                                                                                         Human leukocyte antigen, HLA-A29, tumour rejection antigen, detection, therapy, pathological condition, cancer; CTL; cytolytic T lymphocyte; GAGE; ss.
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AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC
                                   AGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTTGTTCA
                                                                 AGIGITAAAAGAAGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated peptides which bind to HLA-A29 molecules, which are rejection antigens used for detection and therapy of pathological conditions, e.g. cancer.
                                                                                                                                    532
                                                                                                    TIBABARTICICCCAAIBAAGCITIBCAGCCTICIGCAAAAAAAAAAAAAA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boon-Falleur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                    Length 538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        GAGE-2 tumour rejection antigen clone nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 510.2; DB 2;
Pred. No. 1.8e-133;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Den Eynde
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                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid molecule and the isolated nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents CDNA encoding the human GAGB-7B polypeptide of the invention. The gene resides on chromosome Xpll.2-pll.4.
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                                                                                                                                                                                                                               Score 504; DB 7; Length 526;
Pred. No. 1e-131;
); Mismatches 5; Indels
                                                                                                                                                                                                      Sequence 526 BP; 168 A; 109 C; 143 G; 106 T; 0 U; 0 Other;
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298 CAGGAACAGGGTCACCCACAGACTGGGTGTGTGTGTGAAGATGGTCCTGATGGGCAGGAG 357
              Local Similarity 98.1
les 520; Conservative
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                                                                                                                                                                                                                                                                                                                             Human; GAGE-8; gene; ss; cytolytic T lymphocyte; CTL;
human leukocyte antigen; HLA; tumour rejection antigen precursor;
major histocompatibility complex; MHC; cytolytic T cell proliferation;
chromosome Xpl1.2-pl1.4.
                                                                                                                                                                                                    ADA15801 standard; cDNA; 528
                                                                                                                                                                                                                                                                 (first entry)
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Homo sapiens

06-NOV-2003

Human

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New GAGE-7B and GAGE-8 nucleic acid molecules, useful in coding for tumor rejection antigen precursors, which complex to major histocompatibility complex molecules to facilitate the proliferation of cytolytic T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated GAGE-7B and GAGE-8 polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid molecules encoding them. The invention also relates to an expression vector comprising an isolated nucleic acid molecule of the invention operably linked to a promoter, a recombinant cell comprising the isolated nucleic acid molecule or the expression vector and an expression kit useful in generating cytolytic T lymphocytes (CTLs) or determining if CTLs are present in a sample comprising the isolated nucleic acid molecule and the isolated nucleic acid molecule and the isolated nucleic acid molecule and the isolated nucleic acid molecules encode tumour rejection antigen precursors, which complex to major histocompatibility complex (MHC) molecules to facilitate the proliferation of cytolytic T cells. This sequence represents cDNA encoding the human GAGE-8 polypeptide of the invention. The gene resides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 TCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTAATTATTGGCCTAGACCAAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 528 BP; 158 A; 112 C; 151 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                           aa:Gln)
aa:Lys)
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                                                                                           /transl_except= (pos:244. .246, /transl_except= (pos:400. .402,
                                                                                                                                                                                                                                                                                                                                                                                                Boon-Falleur T;
  Location/Qualifiers
                                                                   'product= "Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 7-10; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
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GGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAG 420
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 GCCAGGGAGCTGTGAGGCAGTGCTGTGTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTAC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid encoding GAGE tumour rejection antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA
                                                           TGAGATICATCTGTGTGAAATATGAGTGGGGAGGAAGATGCGC---TATCGGCCTAGA
                                                                                                              CCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCCTATGCGGCCCCGAGCAGTTCAGT
                                                                                                                                         120 CCAAGACGCTACGTAGAGCCTCCTGAAATGATTGATTGGGGCCTATGCGGCCCGAGGCAGTTCAGT
                                                                                                                                                                                                                                                                                                                                      GCTGATAGCCAGGAACAGGGTCACCCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGAT
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                                                                                                                                                                                                                          180 GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGGAACCAGCAACTCAACGTCAGGATCCT
                                                                                                                                                                                                                                                             GCAGCTGCTCAGGAGGGAGAGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding GAGE-2 tumour rejection antigen precursor.
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aa:Thr)
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(pos:195.
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P-PSDB; AAW47599.
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                                    417
                                                                           489
                                                                                                              477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic polynuclectides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cancer; tumour; therapy; diagnosis; CT antigen; CP antigen; immune response; virology; immunology; microbiology; molecular biology; recombinant DNA technology; gene; ss.
                                                                                              TGTTAAAAAGAAGAACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATT
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370 GTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAG
                                  358 ATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAG
                                                                         TGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATT
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                                                                                                                                                  530 BP; 152 A; 116 C; 155 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 502.2; DB 7; ilarity 97.9%; Pred. No. 3.3e-131; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                        GAGE-2 full length cDNA sequence SEQ ID NO:2890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2890; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaiger A;
                                                                                                                                                                                                                                                                                BP
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28-AUG-2001; 2001US-0315563P.
09-JAN-2002; 2002US-0347313P.
                                                                                                                                                                                                                                                                              ABZ20463 standard; cDNA; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR~2002; 2002WO-US010421
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity
Matches 520; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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techniques.
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The present sequence encodes a GAGE-2 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally calferent from the other GAGE CDMAs for the first 112 bases. This region of GAGE-3 cDMA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other was for the processed peptides, include HLA-typing assays for,
   processed by HLA-Cw6 molecules into peptides, useful to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. skin graft or organ transplants
                                                                                            Example 13; Fig 4; 60pp; English
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8 Length 535; Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 U; 0 Other; Indels DB 2; 1.1e-121; ches 16; 0; Mismatches Score 468.4; Pred. No. 1.1 86.9%; Conservative Local Similarity Matches 516; Query Match

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1 GCCAGGGAGCTGTGAGGCAGTGCTGTGTGTTCCTGCCGTCCGGGACTCTTTTCCTC-TA
                             GCCAGGGAGCTGTGAGGCAGTGCTGTG----TTCTTGCGTCCGGACTCTTTTTCCTTTA
                                                       CTGAGATTCATCTGTGTAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAG
                                                                                 creadarrearcrereaaarareagrideceaagaacaace---raregecerae
                                                                                                             120 ACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAG
                                                                                                                                     ACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAG
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AAC02129 standard; cDNA; 430
                                                               06-OCT-2000 (first entry)
                                          AAC02129
RESULT 12
AAC02129
ID AAC02:
XX
AC AAC02:
DT 06-OC'
XX
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; expressed sequence tag, secreted protein; cDNA isolation; chromosome mapping; ss. New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures. Claim 1; SEQ ID NO 2127; 71pp + Sequence Listing; English. Giordano J; Human secreted protein 5' EST, SEQ ID NO: 2127 Duclert A, 21-FEB-2000; 2000EP-00200610. 99US-0122487P. Dumas Milne Edwards J, WPI; 2000-500381/45. P-PSDB; AAG02123. EST; (GEST) GENSET Human; 5' EST; gene therapy; Homo sapiens. EP1033401-A2 26-FEB-1999;

The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion

-1 115 120 174 240 GCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA 300 294 9 56 GCCAGGGGAGCTGTGTGTGTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTAC TGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 295 GCAGCTGCTCAGRAGGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGGAAGCCTGAA 1 GCCAGGGAGCTGTGAGGCAGTGCTGTGGGTTCCTGCCGTCCGGACTCTTTTTCCTCTAC 116 TGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATNA-YGGCCTAGA CCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGGCCTATGCGGCCCGAGCAGTTCAGT 175 CCAAGRCGCTATGTACAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGT GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT 235 GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAAYGTCAGGATCCT Gaps 1; Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 0 U; 8 Other; Indels 4; DB 3; 66.1%; Score 356.2; DB 3 97.3%; Pred. No. 4.1e-90; 5; Mismatches Matches 366; Conservative Similarity 61 121 Query Match 181 Local g $\stackrel{>}{\circ}$ 임 Пp qq g δ δ à

GCTGATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGAT 360

301

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355 GCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGGTGGTGGTCCTGAT 414

389 ATCCTGNAGCTGCNCAGNAGGGANAGGATNAGGGNGCATNTGCAGGTCAAGGGCCGAAGC 330

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the used to detect transcripts or genomic sequences corresponding to the carkers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic
                                                                                                                                                                                                                                                                                      uman; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma; quamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia; ymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid, used as a marker to determine the effectiveness of using TAXOL to treat cancer cell growth in individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%; Score 303; DB 4; Length 530; 88.2%; Pred. No. 4.4e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 0 U; 52 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Huffel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                    Human cancer agent-sensitive marker #105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 120; 527pp; English.
                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                     Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bolt A,
                                    GGGCAGGAGATGGAMC 430
                                                                                                                                    AAS60104 standard; cDNA; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-2001; 2001WO-US012132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-2000; 2000US-0197538P
                                                                                                                                                                                                               (first entry)
GGGCAGGAGGTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-602933/68.
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179556-A2.
                                                                                                                                                                                                                                                                                                               squamous cell
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                               29-JAN-2002
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                                                                                               RESULT 13
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The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the articancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the
                                 CTGAAGNTGATAGCCAGGAACAGGGTCNCCCCANACTGGGNGTNAGTGTNAAAATGGTC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ncer cell marker; TAXOL; cytostatic; tumour; carcinoma;
cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
c leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid, used as a marker to determine the effectiveness of TAXOL to treat cancer cell growth in individuals.
                                                                                                                                                                                                                                                     CTGATGGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTG
                                                                                                                                                                                        AAAAGCAATCCCAGTGTTAAAANAAGGCNCGTTGAAATGATGCAGGCTGCTCCTATGTTG
CTGAAGCTGATAGCCAGGAACAGGGTCACCCCACAGACTGGGTGTGTGAAGATGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Huffel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer agent-sensitive marker #227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS60496 standard; cDNA; 365 BP.
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235 390 295

Gaps

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Indels

41;

Mismatches

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Best Local Similarity 88.2 Matches 321; Conservative

Similarity

178 AGTGATGAAGTGGAACCAGC--AACACCTGAAGAAGGGGGAACCAGCAACTCAACGTCAGG

ATCCTGCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New immunogenic polynucleotides or polypeptides useful for diagnosing, betwenting and treating cancer expressing CT or CP mRNA antigens, and in virology, immunology, microbiology, molecular biology and recombinant DNA techniques.
            cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers
                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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 Cancers which may be targeted include carcinoma (e.g. squamous
                                                                                                                                                                                                      GCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAAAGGATAAGGGAGCATCTGCA
                                                                                                                                                                                                                                     GGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAGGGTCACCCCACAGACTGGGTGT
                                                                                                                                                                                                                                                                                             GAGTGTGAAGATGGTCCTGATGGGCAGGAGGTGGACCCGCCAAATCCAGAGGAGGTGAAA
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                                                                                                                    DB 4; Length 365;
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                                                                                     Sequence 365 BP; 63 A; 86 C; 66 G; 150 T; 0 U; 0 Other;
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                                                                                                                  Score 300.8; DB 4
Pred. No. 1.6e-74;
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ABD17575 to ABD20506 represent isolated polynucleotide (I) sequences, and ABD54446 to ABD54472 represent protein (II) sequences, from the present invention. (I) and (II) have cytostatic activity and can be used in gene therapy and vaccines. (I) (II), intibodies and compositions from the present invention are useful for diagnosing, preventing and treating cancer, which expresses CT or CP mRNA antigens. They are useful for stimulating immune response. They can also be useful in virology, immunology, microbiology, molecular biology and recombinant DNA techniques. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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Pred. No. 1.4e-58;
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nes 244; Conservative
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Job time: 395 secs
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